

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:12:36 ; Search time 74 Seconds  
(without alignments)  
1829.272 Million cell updates/sec

Title: US-09-721-341-2  
Perfect score: 1819  
Sequence: 1 MALEQNQSTDYENEMNG.....VEPPFDSEGPTEPTSTFSI 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	AAW93169 Human HPI
2	1819	100.0	350	2	AAW93169 Human HPI
3	1819	100.0	350	2	AAW93169 Human HPI
4	1819	100.0	350	2	AAW93169 Human HPI
5	1819	100.0	350	2	AAW93169 Human HPI
6	1819	100.0	350	2	AAW93169 Human HPI
7	1819	100.0	350	2	AAW93169 Human HPI
8	1819	100.0	350	2	AAW93169 Human HPI
9	1819	100.0	350	2	AAW93169 Human HPI
10	1819	100.0	350	2	AAW93169 Human HPI
11	1819	100.0	350	2	AAW93169 Human HPI
12	1819	100.0	350	2	AAW93169 Human HPI
13	1819	100.0	350	2	AAW93169 Human HPI
14	1819	100.0	350	2	AAW93169 Human HPI
15	1819	100.0	350	2	AAW93169 Human HPI
16	1819	100.0	350	2	AAW93169 Human HPI
17	1819	100.0	350	2	AAW93169 Human HPI
18	1819	100.0	350	2	AAW93169 Human HPI
19	1819	100.0	350	2	AAW93169 Human HPI
20	1819	100.0	350	2	AAW93169 Human HPI
21	1819	100.0	350	2	AAW93169 Human HPI
22	1819	100.0	350	2	AAW93169 Human HPI
23	1819	100.0	350	2	AAW93169 Human HPI
24	1819	100.0	350	2	AAW93169 Human HPI
25	1819	100.0	350	2	AAW93169 Human HPI

26	1810	99.5	350	8	ADQ75082 Human G P
27	1808	99.4	350	3	AA837788 Human TSC
28	1804	99.2	350	8	ADG65525 Human end
29	1803	99.1	350	7	ADP60895 Human GPC
30	1728	95.0	333	2	AA57289 Human BGC
31	1620	89.1	350	4	AA67238 Human BGC
32	1620	89.1	350	7	ADA10817 Cow signa
33	1593	87.6	350	8	ADO29238 Mouse GPC
34	1591	87.5	350	2	AA57291 Mouse BGC
35	1275	70.1	246	2	AA57292 Human BGC
36	1257	69.1	242	4	AAW99949 Human exp
37	1212	66.6	263	2	AA570126 A seven-P
38	862	47.4	164	4	AB111162 Human orp
39	862	47.4	164	4	AAW79310 Human pro
40	824	45.3	159	3	AA841786 Human ORF
41	761	41.8	175	4	AAU18115 Novel hum
42	761	41.8	175	4	AAU18669 Renal and
43	761	41.8	175	4	AAU21655 Novel hum
44	761	41.8	175	4	AAW99976 Human exp
45	761	41.8	175	4	AB110276 Human CDN

#### ALIGNMENTS

RESULT 1	AAW93169	standard; protein; 350 AA.
ID	AAW93169	
XX	AAW93169;	
AC		
XX		
DT	24-MAY-1999	(first entry)
XX		
DE	Human HPIA041 protein.	
XX		
KW	HPIA041; G-coupled receptor; disease susceptibility; diagnosis; immunise;	
KW	treatment; FIA041 protein; gene therapy; immune response; vaccine; HIV-2;	
KW	inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;	
KW	diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;	
KW	hypotension; hypertension; urinary retention; osteoporosis; allergy;	
KW	angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;	
KW	benign prostatic hyperplasia; psychotic disorder; neurological disorder;	
KW	anxiety; manic depression; delirium; dementia; severe mental retardation;	
KW	dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;	
KW	linkage analysis; gene mapping; human.	
XX		
OS	Homo sapiens.	
XX		
PN	EP899332-A2.	
XX		
PD	03-MAR-1999.	
XX		
XX		
PF	17-FEB-1998; 98EP-00301170.	
XX		
PR	15-AUG-1997; 97US-0055895P.	
XX		
PR	27-OCT-1997; 97US-00962922.	
XX		
PA	(SMIX ) SMITHKLINE BEECHAM CORP.	
XX		
PI	Ellis CE;	
XX		
DR	WPI: 1999-144803/13.	
XX		
DR	N-PSDB; AA22557.	
XX		
PT	New G-coupled receptor (HPIA041) polypeptide and polynucleotide - useful	
XX	as diagnostic reagents and for prevention and treatment of cancer, HIV	
PT	infections and Parkinson's disease.	
XX		
PS	Claim 1; Page 22-23; 27pp; English.	
XX		
CC	This sequence represents a G-coupled receptor, HPIA041 which is useful	
XX	for diagnosing susceptibility to diseases by detecting mutations in the	
CC	HPIA041 gene, and can diagnose diseases associated with HPIA041 protein	

CC imbalance by determining HPIA041 polypeptide expression levels. Agonists  
 CC and antagonists of the protein can be used in treatment to activate  
 CC (agonist) or inhibit (antagonist) HPIA041 activity, in addition to direct  
 CC administration of antisense sequences to prevent expression, or HPIA041  
 CC polynucleotides to treat conditions associated with a lack of HPIA041  
 CC protein. Gene therapy may also be used to affect endogenous HPIA041  
 CC polypeptide expression. HPIA041 antibodies are useful for inducing an  
 CC immune response to immune and prevent disease, and for isolating  
 CC HPIA041 clones or purifying the polypeptides by affinity chromatography.  
 CC HPIA041 polypeptides can be administered directly or as a vaccine to  
 CC inoculate against disease. Diseases diagnosed, prevented and treated  
 CC include bacterial, fungal, protozoan and viral infections, particularly  
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's  
 CC disease; acute heart failure; hypotension; hypertension; urinary  
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;  
 CC asthma; allergies; benign prostatic hypertrophy; and psychotic and  
 CC neurological disorders, including anxiety, schizophrenia, manic  
 CC depression, delirium, dementia, severe mental retardation and dyskinesias  
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The  
 CC HPIA041 polypeptide is also useful for mapping the gene to a chromosome,  
 CC allowing gene inheritance to be studied through linkage analysis  
 CC

SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKFLPVLITVPIGAGNS 60  
 DB 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKFLPVLITVPIGAGNS 60  
 QY 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 DB 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 QY 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 DB 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 QY 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNPKISRPLK 240  
 DB 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNPKISRPLK 240  
 QY 241 VLLTVYIVIVTQLPYNIYKFCRAIDIIYSLITSCKMSKRMIDIAIQTESIAlFHSCLNP 300  
 DB 241 VLLTVYIVIVTQLPYNIYKFCRAIDIIYSLITSCKMSKRMIDIAIQTESIAlFHSCLNP 300  
 QY 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350

RESULT 2  
 AAY17435  
 ID AAY17435 standard; protein; 350 AA.

AC AAY17435;  
 XX 29-JUL-1999 (first entry)  
 DT Human signal peptide-containing protein SP-16.  
 DE Human signal peptide-containing protein SP-16.  
 XX Human; signal peptide-containing protein; SP; cell proliferation; cancer;  
 KM neuronal disorder; immune response; detection.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO924463-A2.  
 PN 20-MAY-1999.  
 PD 04-NOV-1998; 98WO-US023578.  
 XX PF

XX 07-NOV-1997; 97US-00966316.  
 PR (INCY-) INCYTE PHARM INC.  
 XX  
 PA Lal P, Au-Young J, Reddy R, Murry LE, Mathur P;  
 PI WPI; 1999-337694/28.  
 DR N-PSDB; AAX61288.  
 XX  
 PT CDNA clones encoding signal peptide-containing proteins.  
 PS Claim 1; Fig 1; 83pp; English.  
 XX  
 CC The present sequence represents a human signal peptide-containing protein  
 CC (SP), designated SP-16. SP proteins can be used to stimulate cell  
 CC proliferation or to treat or prevent cancer. SP antagonists are also used  
 CC to treat or prevent cancer, and also for treating or preventing neuronal  
 CC disorders or immune responses. Polynucleotide sequences complementary to  
 CC the SP-encoding polynucleotides are useful for the detection of SP-  
 CC encoding nucleic acid molecules in biological samples  
 CC

SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKFLPVLITVPIGAGNS 60  
 DB 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKFLPVLITVPIGAGNS 60  
 QY 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 DB 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 QY 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 DB 61 MVAIAYAYKKKORTKTDVYIILNLAADVLLFLTPFMAVNAVHGWLGKIMCKITSALYT 120  
 QY 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 INFVSGMOFLACISIDRYAVAVTKVPSQSGVGRPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNPKISRPLK 240  
 DB 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNPKISRPLK 240  
 QY 241 VLLTVYIVIVTQLPYNIYKFCRAIDIIYSLITSCKMSKRMIDIAIQTESIAlFHSCLNP 300  
 DB 241 VLLTVYIVIVTQLPYNIYKFCRAIDIIYSLITSCKMSKRMIDIAIQTESIAlFHSCLNP 300  
 QY 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350

RESULT 3  
 AAY57290  
 ID AAY57290 standard; protein; 350 AA.

AC AAY57290;  
 XX 05-JUN-2000 (first entry)  
 DT Human BGCKr protein.  
 DE Human BGCKr protein.  
 XX BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;  
 KM cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;  
 KW anti-allergic; antiviral.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO952945-A2.  
 PN 21-OCT-1999.  
 PD XX

PF 16-APR-1999; 99WO-US008395.  
 XX  
 PR 16-APR-1998; 98US-00061753.  
 PR 16-APR-1999; 99US-00061753.  
 XX  
 PA (MILL-) MILLENITUM PHARM INC.  
 XX  
 PI Gonzalo JA, Gutierrez-Ramos JC;  
 XX  
 DR WPI, 1999-620375/53.  
 DR N-PSDB; AA290528.  
 PT New nucleic acid encoding human BGCKr receptor, used e.g. for modulating  
 PT inflammation and tumor growth.  
 XX  
 PS Claim 8; Fig 2A-B; 123pp; English.  
 XX  
 CC The invention relates to a human BGCKr protein, a G-protein coupled  
 CC receptor. The BGCKr protein can be expressed by standard recombinant  
 CC methodology. BGCKr are receptor proteins possibly involved in modulation  
 CC of proinflammatory or stimulatory functions of chemokines, cell  
 CC proliferation, migration, adhesion and targeting, and exocytosis. The  
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies  
 CC and modulators are potentially useful for modulating inflammation;  
 CC chemotactic activity of leucocytes; angiogenesis; cell proliferation;  
 CC tumour growth; allergic reactions and entry of human immune deficiency  
 CC virus into cells, for therapeutic or prophylactic purposes. They are also  
 CC used for diagnosis and in drug-screening assays. The present sequence  
 CC represents the full-length human BGCKr protein  
 XX  
 SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPEPLTIVPIGAGNS 60  
 DB 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPEPLTIVPIGAGNS 60  
 DB 61 MVAIAYYYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120  
 DB 61 MVAIAYYYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120  
 DB 61 MVAIAYYYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120  
 OY 121 LNFVSGMOLACISIRYAVATKVPQSQSGKRCWICFCVMAAIIILSTPOLVFTYND 180  
 DB 121 LNFVSGMOLACISIRYAVATKVPQSQSGKRCWICFCVMAAIIILSTPOLVFTYND 180  
 OY 181 NARCIPFRVYLGTSKMKALIQMLEICIGFVVPFLINGVCYFTRARTLMKPNKISRPLK 240  
 DB 181 NARCIPFRVYLGTSKMKALIQMLEICIGFVVPFLINGVCYFTRARTLMKPNKISRPLK 240  
 OY 241 VLLTVIVIVITQLPNYIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSGLNP 300  
 DB 241 VLLTVIVIVITQLPNYIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSGLNP 300  
 OY 301 ILYVFGASFPKYNVMYAKKYGSROROSVEEFPDSEPTPTSTFSI 350  
 DB 301 ILYVFGASFPKYNVMYAKKYGSROROSVEEFPDSEPTPTSTFSI 350

RESULT 4  
 AA94325  
 ID AA94325 standard; proteoin; 350 AA.  
 XX  
 AC AA94325;  
 XX  
 DT 11-AUG-2000 (first entry)  
 XX  
 DE Human seven transmembrane receptor VSHK-1.  
 XX  
 KW Human; seven transmembrane receptor; VSHK-1; signal transduction.  
 XX

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6..8  
 FT /note= "potential N-glycosylation site"  
 FT 19..21  
 FT Modified-site  
 FT /note= "potential N-glycosylation site"  
 FT 42..66  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 79..100  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 114..135  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 156..175  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 199..221  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 241..262  
 FT Domain  
 FT /label= Transmembrane\_domain  
 FT 276..278  
 FT Modified-site  
 FT /note= "potential N-glycosylation site"  
 FT 287..308  
 FT Domain  
 FT /label= Transmembrane\_domain  
 PD WO200026369-A1.  
 PD 11-MAY-2000.  
 PP 03-NOV-1999; 99WO-US025848.  
 PP  
 PR 04-NOV-1998; 98US-0107112P.  
 PR 06-JAN-1999; 99US-0114856P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Khoja H, Shymala V;  
 XX  
 DR WPI; 2000-365618/31.  
 DR N-PSDB; AA94325.  
 PT Novel polypeptide comprising a new seven-transmembrane receptor protein  
 PT and its encoding polynucleotide, useful for the analysis of VSHK-1.  
 XX  
 PS Claim 3; Fig 1; 79pp; English.

XX The present sequence is VSHK-1, a new seven transmembrane receptor which  
 CC contains seven membrane-spanning helical domains that are linked by three  
 CC intracellular and three extracellular loops. The gene sequence encoding  
 CC VSHK-1 was isolated from a cDNA library. In heart tissue, where VSHK-1 is  
 CC predominantly found, three RNA species were identified: a 1.3kb, a 2.0kb,  
 CC and a 5.0kb species. The polynucleotide encoding the present sequence  
 CC corresponds to the 2.0kb form. The 1.3kb form may result from the use of  
 CC an alternative polyadenylation site while transcription of a 3.0kb intron  
 CC at nucleotide 74 could account for the 5.0kb species. VSHK-1  
 CC polynucleotides can be used as hybridisation probes to detect and measure  
 CC VSHK-1 mRNA. They may also be used to identify substances that modulate  
 CC the level of VSHK-1 mRNA. The VSHK-1 coding sequence can be integrated  
 CC into an expression vector for production of VSHK-1 receptor polypeptides  
 CC in host cells. The polypeptides can be used to identify agents which  
 CC modulate VSHK-1 receptor signal transduction activity  
 XX

SQ Sequence 350 AA;  
 Query Match 100.0%; Score 1819; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPEPLTIVPIGAGNS 60  
 DB 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPEPLTIVPIGAGNS 60  
 OY 61 MVAIAYYYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWLGKIMCKITSALYT 120  
 |||

Db 61 MVAIAYKKORTKTDVYILMLAVADLLFLPFWANAVHGWLGKIMCKITSALYT 120

Qy 121 LNFVSGMOPLACISIDRYAVATKVPBSQGVGKPCWIIICCVMAAILLSIPOLVFYTVND 180

Db 121 LNFVSGMOPLACISIDRYAVATKVPBSQGVGKPCWIIICCVMAAILLSIPOLVFYTVND 180

Qy 181 NARCIPIFPRYLGTSKALIQMLEICIGFVVPFLINGVCYFITARTLMKMPNIIKISRPLK 240

Db 181 NARCIPIFPRYLGTSKALIQMLEICIGFVVPFLINGVCYFITARTLMKMPNIIKISRPLK 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMMDIAIQVTSIALFHSCLNP 300

Db 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMMDIAIQVTSIALFHSCLNP 300

Qy 301 ILVFMGASFKYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

Db 301 ILVFMGASFKYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

## RESULT 5

AAU08994 standard; protein; 350 AA.

AAU08994;

18-DEC-2001 (first entry)

Human G protein-coupled receptor, GPCR, 2398.

Human; GPCR; G protein-coupled receptor; 2398; cardiac; antiatherosclerotic; analgesic; cyostatic; antianginal; cardiovascular disorder; angiogenesis-related disorder; neural disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; ischemic heart disease; sudden cardiac death; obesity; hypertensive heart disease; diabetes; prostate cancer-related pain.

Homo sapiens.

Location/Qualifiers

125..141

/label=G\_protein\_receptor\_signature

WO200164882-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US006543.

29-FEB-2000; 2000US-0186059P.

(MILL-) MILLENNIUM PHARM INC.

Glucksman MA, Galvin KM, Silos-Santiago I,

WPI; 2001-589866/66.

N-PSDB; AAS14572.

Novel G protein coupled receptors and nucleic acids encoding them, for identifying agents for the treatment of cardiac disorders.

Claim 9; Fig 9; 209pp; English.

The invention relates to novel human G protein-coupled receptors (GPCR) named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and nucleic acids encoding them are useful for identifying agents for the treatment of cardiovascular disorders, angiogenesis-related disorders, neural disorders, pain response disorders and inflammatory disorders e.g. atherosclerosis, angina pectoris and myocardial infarction, ischemic heart disease, sudden cardiac death, hypertensive heart disease, diabetes, prostate cancer-related pain, diabetes and obesity. The present sequence represents GPCR 2398

SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;

Best Local Similarity 100.0%; Pred. No. 1..1e-194; Mismatches 0; Gaps 0;

Matches 350; Conservative 0; Indels 0; Gaps 0;

Qy 1 MLEQNSQSTDYEEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60

Db 1 MLEQNSQSTDYEEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60

Qy 61 MVAIAYKKORTKTDVYILMLAVADLLFLPFWANAVHGWLGKIMCKITSALYT 120

Db 61 MVAIAYKKORTKTDVYILMLAVADLLFLPFWANAVHGWLGKIMCKITSALYT 120

Qy 121 LNFVSGMOPLACISIDRYAVATKVPBSQGVGKPCWIIICCVMAAILLSIPOLVFYTVND 180

Db 121 LNFVSGMOPLACISIDRYAVATKVPBSQGVGKPCWIIICCVMAAILLSIPOLVFYTVND 180

Qy 181 NARCIPIFPRYLGTSKALIQMLEICIGFVVPFLINGVCYFITARTLMKMPNIIKISRPLK 240

Db 181 NARCIPIFPRYLGTSKALIQMLEICIGFVVPFLINGVCYFITARTLMKMPNIIKISRPLK 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMMDIAIQVTSIALFHSCLNP 300

Db 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMMDIAIQVTSIALFHSCLNP 300

Qy 301 ILVFMGASFKYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

Db 301 ILVFMGASFKYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

## RESULT 6

AAAG80119 standard; protein; 350 AA.

AAAG80119;

17-JAN-2002 (first entry)

Human CCR11 protein.

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antiaesthetic; immunosuppressive; dermatological; antirheumatic; antiarthritic.

Homo sapiens.

WO200172830-A2.

04-OCT-2001.

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

(IPFP-) IPF PHARM GMBH.

(FORS/) FORSMANN U.

Forsmann W, Adermann K, Heitland A, Spodeberg N;

WPI; 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Disclosure; Page 11; 26pp; German.

This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal

or prostatic), organ rejection, inflammation and autoimmune diseases.  
 CC Also inhibitors of (i) are used therapeutically against tumors (and their  
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
 CC endocrine, motor or urogenital systems or skin are affected, and bone  
 CC marrow diseases. The products of the invention are chemokine derivatives  
 CC which have cytostatic, antiinflammatory, antiasclerotic,  
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic,  
 CC chemokines act on specific tumor and inflammatory cells through a  
 CC stimulation of chemokine receptors (CR), which control migration and  
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
 CC fragments used to illustrate the method of the invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLEQNOSTDYVEENENMGTYDSQYELICKEVDREFAKFLVPLTIVVIGLAGNS 60  
 Db 1 MLEQNOSTDYVEENENMGTYDSQYELICKEVDREFAKFLVPLTIVVIGLAGNS 60  
 Qy 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVVLGKIMCKITSALT 120  
 Db 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVVLGKIMCKITSALT 120  
 Qy 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180  
 Db 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180

Qy 181 NARCIPIPRRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTTARTLMKMPNPKISRPK 240  
 Db 181 NARCIPIPRRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTTARTLMKMPNPKISRPK 240  
 Qy 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVESIALFHSCLNP 300  
 Db 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVESIALFHSCLNP 300

Qy 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350  
 Db 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

RESULT 7  
 AAG67237  
 ID AAG67237 standard; protein; 350 AA.

XX AAG67237;

DT 13-NOV-2001 (first entry)

XX Amino acid sequence of human chemokine receptor CCR11.

XX Human; chemokine receptor; CCR11; G protein coupled receptor;  
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;  
 KW asthma; angiodenesis; atherosclerosis vascular association disease;  
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;  
 KW left ventricular diastolic dysfunction; migraine; preterm labour;  
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;  
 KW myocardial infarction; congestive heart failure; endometriosis;  
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

XX Homo sapiens.

XX WO200166598-A2.

XX 13-SEP-2001.

XX 05-MAR-2001; 2001WO-US007073.

XX 03-MAR-2000; 2000US-0186928P.

PR 03-MAR-2000; 2000US-0187231P.

XX (ICOS-) ICOS CORP.

XX Gray PW, Schweickart VL, Bpp A, Raport CJ, Chantry D, Steiner B;

DR WPI; 2001-541918/60.

XX N-PSDB; AAH77711.

PT An isolated polynucleotide encoding the chemokine receptor CCR11, useful  
 PT for treating rheumatoid arthritis, inflammatory bowel disease, asthma,  
 PT angiodenesis, atherosclerosis, cardiac arrhythmias, Raynaud's phenomenon  
 PT and migraine.

XX Claim 13; Page 96-97; 110pp; English.

XX The present sequence represents the human chemokine receptor CCR11. CCR11  
 CC is a member of the G protein coupled receptor family. A CCR11  
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11  
 CC expression or biological activity, is useful for treating many  
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory  
 CC bowel disease, and asthma. They are also useful for treating  
 CC angiodenesis, atherosclerosis vascular association diseases which may  
 CC include but are not limited to hypertension, angina pectoris, cardiac  
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's  
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic  
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive heart  
 CC failure, endometriosis, vasospasm, retinopathy, nephropathy, or pulmonary  
 CC vascular disease

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLEQNOSTDYVEENENMGTYDSQYELICKEVDREFAKFLVPLTIVVIGLAGNS 60  
 Db 1 MLEQNOSTDYVEENENMGTYDSQYELICKEVDREFAKFLVPLTIVVIGLAGNS 60

Qy 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVVLGKIMCKITSALT 120  
 Db 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVVLGKIMCKITSALT 120

Qy 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180  
 Db 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180

Qy 181 NARCIPIPRRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTTARTLMKMPNPKISRPK 240  
 Db 181 NARCIPIPRRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTTARTLMKMPNPKISRPK 240

Qy 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVESIALFHSCLNP 300  
 Db 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVESIALFHSCLNP 300

Qy 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350  
 Db 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

RESULT 8  
 AAE37348  
 ID AAE37348 standard; protein; 350 AA.

XX AAE37348;

XX 27-AUG-2003 (first entry)

XX Human C-C chemokine receptor type 11 (CC CKR-11), 2398 protein.

XX Human; cardiovascular disorder; coronary artery disease; bradycardia;  
 KW stenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina;

KM arteriosclerosis; coronary artery ligation; rheumatic heart disease;  
 KM heart failure; hypertension; cardiomyopathy; myocardial infarction;  
 KM arterial inflammation; microembolism; atherosclerosis; endocarditis;  
 KM vascular heart disease; valvular disease; arrhythmia; gene therapy;  
 KM sinus node dysfunction; C-C chemokine receptor type 11; CC CR-11;  
 KM receptor.  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO2003039341-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 05-NOV-2002; 2002WO-US035538.  
 XX  
 PR 05-NOV-2001; 2001US-0339582P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Logan TJ, Chun M, Galvin KM;  
 XX  
 DR WPI: 2003-441437/41.  
 XX  
 DR N-PSDB; AAD56515.  
 XX  
 PT Treating a subject having a cardiovascular disorder, e.g. angina,  
 PT arrhythmia, or restenosis, comprises administering a 139, 258, 1261,  
 PT 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248 or  
 PT 93804 modulator.  
 XX  
 PS Disclosure; Page 105-106; 124pp; English.  
 XX  
 CC The invention relates to methods and compositions for treating a subject  
 CC having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414,  
 CC 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator.  
 CC The invention is useful for treating a cardiovascular disorder, including  
 CC arteriosclerosis, atherosclerosis, vascular wall remodeling, restenosis,  
 CC cardiac hypertrophy, ischemia reperfusion injury, arterial inflammation,  
 CC ventricular remodeling, rapid ventricular pacing, tachycardia, coronary  
 CC microembolism, bradycardia, pressure overload, aortic bending, coronary  
 CC artery ligation, vascular heart disease, valvular disease, including but  
 CC not limited to, valvular degeneration caused by calcification, rheumatic  
 CC heart disease, endocarditis, or complications of artificial valves;  
 CC atrial fibrillation, long-QT syndrome, congestive heart failure, sinus  
 CC node dysfunction, angina, heart failure, hypertension, atrial flutter,  
 CC atrial fibrillation, pericardial disease, including but not limited to  
 CC pericardial effusion and pericarditis, cardiomyopathies (e.g. dilated  
 CC cardiomyopathy or idiopathic cardiomyopathy), myocardial infarction,  
 CC coronary artery disease, coronary artery spasm, ischemic disease,  
 CC arrhythmia, sudden cardiac death, and cardiovascular developmental  
 CC disorders. The invention is also useful in gene therapy. The present  
 CC sequence is human C-C chemokine receptor type 11 (CC CR-11) protein.  
 CC This sequence is used to illustrate the method of the invention  
 XX  
 XX Sequence 350 AA;  
 SQ

Query Match 100.0%; Score 1819; DB 6; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLEONQSTDDYYEENENNGTDDYSEYELICIKEDYREPAKFLPLPLTLTVPTGLAGNS 60  
 DB 1 MALLEONQSTDDYYEENENNGTDDYSEYELICIKEDYREPAKFLPLPLTLTVPTGLAGNS 60  
 QY 61 MVAATYAYYKKORTKTDVYTLNLAADVLLFLPMAVNAHGWVIGIMCKTTSALT 120  
 DB 61 MVAATYAYYKKORTKTDVYTLNLAADVLLFLPMAVNAHGWVIGIMCKTTSALT 120  
 QY 121 LNFVSGMQFLACISIDRYAVAVTKVPSQSGVKPCWIIICCVMAAILISIPOLVFYTVND 180  
 DB 121 LNFVSGMQFLACISIDRYAVAVTKVPSQSGVKPCWIIICCVMAAILISIPOLVFYTVND 180  
 QY 181 NARCPIDIPRYIGTSKALIQMLEICIGRVVPLIMGVCFYTTARTLMKMPNIKISRP 240  
 DB 181 NARCPIDIPRYIGTSKALIQMLEICIGRVVPLIMGVCFYTTARTLMKMPNIKISRP 240

DB 181 NARCPIDIPRYIGTSKALIQMLEICIGRVVPLIMGVCFYTTARTLMKMPNIKISRP 240  
 QY 241 VLLATVIVFIYVTLQPLPYNIVKFCRAIDITYSILTSQNSMKRMDIAQVETESIALFHSCLNP 300  
 DB 241 VLLATVIVFIYVTLQPLPYNIVKFCRAIDITYSILTSQNSMKRMDIAQVETESIALFHSCLNP 300  
 QY 301 ILVFMGASFNKYVMKVAKKTGSWRQRQSQVEEFPDSEGPPEPTSTSI 350  
 DB 301 ILVFMGASFNKYVMKVAKKTGSWRQRQSQVEEFPDSEGPPEPTSTSI 350  
 RESULT 9  
 ABBP1716  
 ID ABBP1716 standard; protein; 350 AA.  
 XX  
 AC ABBP1716;  
 XX  
 DT 04-MAR-2003 (first entry)  
 XX  
 DE Human C-C chemokine receptor 11 protein SEQ ID NO:607.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; Rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.  
 XX  
 PR 19-DEC-2000; 2000US-0257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burner GC, Roush CL, Brown JP;  
 XX  
 DR WPI: 2003-046718/04.  
 XX  
 DR N-PSDB; ABZ42562.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABBP82019 to ABBP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC regenerating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections, cell  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, proctitis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, ataxia, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 6; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEBQNSTDYEEENKNGTYDYSQYELICKEDEVEFAKVELPVFLTIVFVIGLAGNS 60  
 DB 1 MLEBQNSTDYEEENKNGTYDYSQYELICKEDEVEFAKVELPVFLTIVFVIGLAGNS 60  
 QY 61 MVAATYAYKKKORTKTDVYILNLAVALDLLFTLPFWANVAHGWLGKIMCKITSAALT 120  
 DB 61 MVAATYAYKKKORTKTDVYILNLAVALDLLFTLPFWANVAHGWLGKIMCKITSAALT 120  
 QY 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGKPCWIIICFCVMAAILLSIPOLVFYTVND 180  
 DB 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGKPCWIIICFCVMAAILLSIPOLVFYTVND 180  
 QY 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXISRPXK 240  
 DB 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXISRPXK 240  
 QY 241 VLLTVIVIVITVQLPNTNIVKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300  
 DB 241 VLLTVIVIVITVQLPNTNIVKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300  
 QY 301 ILVVFSGASFKNYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350  
 DB 301 ILVVFSGASFKNYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 10

ADA10754  
 ID ADA10754 standard; protein; 350 AA.

ADA10754;

06-NOV-2003 (first entry)

Human signal peptide containing protein SP-16 Incyte 2547007.

human; signal peptide-containing protein; cell proliferation disorder;  
 cell signaling disorder; Huntington's disease; stomach cancer;  
 uterine cancer; mucinous cystadenoma; arthritis; testicular seminoma;  
 prostate cancer; bladder cancer; renal cell cancer; schizophrenia;  
 asthma; cancer.

Homo sapiens.

US2003073162-A1.

17-APR-2003.

01-OCT-2001; 2001US-00968433.

07-NOV-1997; 97US-00966316.

17-MAR-1999; 99US-00271110.

(LALP/) LAL P. G.  
 (AUTO/) AU-YOUNG J.  
 (REDD/) REDDY R.  
 (MURR/) MURRY L. E.  
 (MATH/) MATHUR P.

XX Lal PG, Au-Young J, Reddy R, Murry LE, Mathur P;  
 XX WPI, 2003-567307/53.  
 XX N-PSDB; ADA10755.  
 DR N-PSDB; ADA10755.  
 PT New signal peptide-containing proteins and nucleic acids, useful in  
 PT diagnosing, prognosing, treating or evaluating therapies for disorders  
 PT associated with cell proliferation and cell signaling.  
 XX Claim 1; Fig 1; 59pp; English.

The invention relates to a new purified signal peptide-containing  
 protein. The signal peptide-containing proteins and nucleic acids  
 encoding them are useful in diagnosing, prognosing, treating or  
 evaluating therapies for disorders associated with cell proliferation and  
 cell signaling such as Huntington's disease, stomach cancer, uterine  
 cancer, mucinous cystadenoma, arthritis, testicular seminoma, prostate  
 cancer, bladder cancer, renal cell cancer, schizophrenia, asthma and  
 cancer. The nucleic acids may be used in hybridization, amplification and  
 screening technologies to identify and distinguish among the identical  
 and related molecules in a sample and to produce transgenic cell lines or  
 organisms which are model systems for cancers and upon which the toxicity  
 and efficacy of potential therapeutic treatments may be tested. The  
 CC present sequence represents the amino acid sequence of a human signal  
 peptide containing protein.

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 7; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEBQNSTDYEEENKNGTYDYSQYELICKEDEVEFAKVELPVFLTIVFVIGLAGNS 60  
 DB 1 MLEBQNSTDYEEENKNGTYDYSQYELICKEDEVEFAKVELPVFLTIVFVIGLAGNS 60  
 QY 61 MVAATYAYKKKORTKTDVYILNLAVALDLLFTLPFWANVAHGWLGKIMCKITSAALT 120  
 DB 61 MVAATYAYKKKORTKTDVYILNLAVALDLLFTLPFWANVAHGWLGKIMCKITSAALT 120  
 QY 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGKPCWIIICFCVMAAILLSIPOLVFYTVND 180  
 DB 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGKPCWIIICFCVMAAILLSIPOLVFYTVND 180  
 QY 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXISRPXK 240  
 DB 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXISRPXK 240  
 QY 241 VLLTVIVIVITVQLPNTNIVKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300  
 DB 241 VLLTVIVIVITVQLPNTNIVKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300  
 QY 301 ILVVFSGASFKNYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350  
 DB 301 ILVVFSGASFKNYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 11

ADG19746  
 ID ADG19746 standard; protein; 350 AA.

ADG19746;

26-FEB-2004 (first entry)

Human G protein coupled receptor (GPCR) 2398.

cytostatic; nephrotoxic; antiinflammatory; cardiac; respiratory;  
 GW gastrotectinal; neuroprotective; angiogenesis stimulator; gene therapy;  
 KW 18636; 2466; 43238; 1983; 52881; 2398; 45449; 50287; 26908;  
 KW cellular proliferative disorder; brain disorder; renal disorder;  
 KW kidney disorder; inflammatory disorder; cardiovascular disorder;



KM liver disorder; intestinal disorder; respiratory disorder;  
 KM angiosenic disorder; human; G protein coupled receptor; GPCR.  
 OS Homo sapiens.  
 FN US2003215860-A1.  
 PD 20-NOV-2003.  
 PF 03-APR-2003; 2003US-00407079.  
 XX  
 PR 29-FEB-2000; 2000US-0186059P.  
 PR 24-MAR-2000; 2000US-0191845P.  
 PR 22-MAY-2000; 2000US-0206019P.  
 PR 17-NOV-2000; 2000US-00715790.  
 PR 28-FEB-2001; 2001US-00796338.  
 PR 22-MAY-2001; 2001US-00863200.  
 PR 22-AUG-2001; 2001US-0314041P.  
 PR 22-AUG-2001; 2001US-0314185P.  
 PR 21-AUG-2002; 2002US-00225094.  
 PR 22-AUG-2002; 2002US-00226102.  
 PR 15-OCT-2002; 2002US-00272417.  
 PR 29-OCT-2002; 2002US-00282837.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM;  
 XX  
 DR WPI: 2004-010777/01.  
 XX  
 DR N-PSDB; ADG19745, ADG19747.  
 XX  
 PT New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,  
 PT 45449, 50289, 52872 or 26908, useful in preparing a composition for  
 PT treating e.g., cellular proliferative, brain, kidney, inflammatory or  
 PT angiogenic disorder.  
 XX  
 PS Claim 4; SEQ ID NO 84; 163bp; English.  
 XX  
 XX The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,  
 CC 2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a  
 CC sequence comprising 939-3489 bp or its fragment comprising at least 15  
 CC nucleotides; a sequence encoding a polypeptide comprising a sequence  
 CC having 223-852 amino acids, or its allelic variant or fragment comprising  
 CC at least 15 contiguous amino acids; or a sequence that hybridises with  
 CC (1) under stringent conditions. The nucleic acid or polypeptide is useful  
 CC in preparing a composition for treating a disorder characterised by  
 CC aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or  
 CC 26908 activity e.g., cellular proliferative, brain, renal, kidney,  
 CC inflammatory, cardiovascular, liver, intestinal, respiratory or  
 CC angiogenic disorder. This is the amino acid sequence of novel human  
 CC protein 2398, a G protein coupled receptor (GPCR).  
 XX  
 SO Sequence 350 AA;  
 Query Match 100.0%; Score 1819; DB 8; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60  
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60  
 QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVNAVAGWVGKIMCKITSAIYT 120  
 DB 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVNAVAGWVGKIMCKITSAIYT 120  
 QY 121 LNFVSGMOFLACISIDRYVAATKVPBSQSGVKRCWIIICFVMAAIIISIPOLVFYTVND 180  
 DB 121 LNFVSGMOFLACISIDRYVAATKVPBSQSGVKRCWIIICFVMAAIIISIPOLVFYTVND 180  
 QY 181 NARCIPFPRYIGTSKAKIOMLEICIGVVPPLINGVCYFITTARTLMKMPNIKISRPK 240  
 DB 181 NARCIPFPRYIGTSKAKIOMLEICIGVVPPLINGVCYFITTARTLMKMPNIKISRPK 240  
 DB 181 NARCIPFPRYIGTSKAKIOMLEICIGVVPPLINGVCYFITTARTLMKMPNIKISRPK 240

QY 241 VLLTFVIVFIYTOLEPYNIIVKFCRAIDIIYSITSCNMSKRMIDIAIQVTESIALFHSCLNP 300  
 DB 241 VLLTFVIVFIYTOLEPYNIIVKFCRAIDIIYSITSCNMSKRMIDIAIQVTESIALFHSCLNP 300  
 QY 301 ILYVFMGASFQKYVWKAKKYGSMRROQSVSEFPDSEGPTEPTSTSI 350  
 DB 301 ILYVFMGASFQKYVWKAKKYGSMRROQSVSEFPDSEGPTEPTSTSI 350  
 RESULT 12  
 ADM46693  
 ID ADM46693 standard; protein; 350 AA.  
 XX  
 AC ADM46693;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human chemokine receptor 11 protein.  
 XX  
 KM screening; therapeutic agent; peripheral; central nervous system;  
 KM cardio-vascular disease; genitourinary; metabolic; haematological;  
 KM chemokine receptor 11; CCR11; uropathic; antianaemic; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1365245-A1.  
 XX  
 PD 26-NOV-2003.  
 XX  
 PF 23-MAY-2002; 2002EP-00011528.  
 XX  
 PR 23-MAY-2002; 2002EP-00011528.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Golz S, Brueggemeier U, Geerts A;  
 XX  
 DR WPI: 2004-024617/03.  
 XX  
 DR N-PSDB; ADM46692.  
 XX  
 PT Screening for therapeutic agents useful for treating nervous system,  
 PT cardiovascular, genitourinary, metabolic or hematological diseases in a  
 PT mammal, by contacting a test compound with a chemokine receptor 11  
 PT polypeptide.  
 XX  
 PS Disclosure; SEQ ID NO 2; 55bp; English.  
 XX  
 CC The invention relates to a novel method for screening for therapeutic  
 CC agents useful for treating diseases. The diseases are chosen from  
 CC disorders of peripheral and central nervous system, cardio-vascular  
 CC disease, genitourinary diseases, metabolic diseases and haematological  
 CC diseases in mammals, by contacting a test compound with a chemokine  
 CC receptor 11 (CCR11) polypeptide and detecting binding of the test  
 CC compound to the CCR11 polypeptide. The therapeutic agents have uropathic  
 CC and antianaemic activities. The invention comprises a further method  
 CC useful for screening for therapeutic agents for treating the same  
 CC diseases that act by binding to a CCR11 polynucleotide. A method is also  
 CC provided for diagnosing the listed diseases. The compositions comprising  
 CC identified therapeutic agents, or the CCR11 polypeptide or polynucleotide  
 CC are useful for treating the diseases. This sequence represents the human  
 CC chemokine receptor 11 protein of the invention.  
 XX  
 SO Sequence 350 AA;  
 Query Match 100.0%; Score 1819; DB 8; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60  
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60



QY 61 MVAIAAYKKORTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGKIMCKITSALYT 120  
 DB 61 MVAIAAYKKORTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGKIMCKITSALYT 120  
 QY 121 LNFVSGMQLACISIDRYVAATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFTYND 180  
 DB 121 LNFVSGMQLACISIDRYVAATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFTYND 180  
 QY 181 NARCPIPFPRYIGTSMKALIQMLEICIGFVPLMGVCYFTTARTLMCKMPNKRPRK 240  
 DB 181 NARCPIPFPRYIGTSMKALIQMLEICIGFVPLMGVCYFTTARTLMCKMPNKRPRK 240  
 QY 241 VLLTVIVIVITQLPNIVKFCRAIDIIISLTSCMSKRMIDIAOVETESIALFHSCLNP 300  
 DB 241 VLLTVIVIVITQLPNIVKFCRAIDIIISLTSCMSKRMIDIAOVETESIALFHSCLNP 300  
 QY 301 ILYVFMGASFKNYVMKAKKYSWRQROSVBEPDSEGPTEPTSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKAKKYSWRQROSVBEPDSEGPTEPTSTFSI 350

## RESULT 13

ADO29237  
 ID ADO29237 standard; protein; 350 AA.

AC ADO29237;

DT 29-JUL-2004 (first entry)

DE Human GPCR CCR1, SEQ ID NO:338.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 XX transgenic mouse; neurological disorder; adrenal gland disorder;  
 XX colon disorder; intestinal disorder; cardiovascular disorder;  
 XX muscular disorder; blood disorder; immune disorder; bone disorder;  
 XX joint disorder; metabolic disorder; nutritive disorder; cancer;  
 XX kidney disorder; liver disorder; lung disorder; breast disorder;  
 XX ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 XX thymus disorder; thyroid disorder; antiparkinsonian; antianemic;  
 XX cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
 XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 XX virostatic; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
 XX dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 XX receptor.

XX Homo sapiens.

OS WO2004040000-A2.

PN 13-MAY-2004.

PF 09-SEP-2003; 2003WO-US028226.

PR 09-SEP-2003; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

PA (PRIM-) PRIMAL INC.

PI Galanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, McLlwain KL, Pavlova MN, Vasiliadis D, Zeng H;

DR WPI; 2004-390329/36.

DR N-PSDB; ADO29837.

XX Novel mammalian G protein coupled receptors, useful for identifying

XX PT compounds that modulates diagnosing and treating disease condition

XX PT associated with GPCR dysfunction e.g. autoimmune diseases, angina

XX PT receptors, Parkinson's disease.

XX PS Claim 151; SEQ ID NO 338; 542pp; English.

CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; method of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridise to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pcr\_sequences.

XX Sequence 350 AA:

SO Query Match 100.0%; Score 1819; DB 8; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEONQSDYYEENENGGTDYSGYELICKEDVREKAKFLPFLITVIVIGLAGNS 60  
 DB 1 MLEONQSDYYEENENGGTDYSGYELICKEDVREKAKFLPFLITVIVIGLAGNS 60  
 QY 61 MVAIAAYKKORTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGKIMCKITSALYT 120  
 DB 61 MVAIAAYKKORTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGKIMCKITSALYT 120  
 QY 121 LNFVSGMQLACISIDRYVAATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFTYND 180  
 DB 121 LNFVSGMQLACISIDRYVAATKVPSSQSGVKPCWIIICFCVMAAILLSIPOLVFTYND 180  
 QY 181 NARCPIPFPRYIGTSMKALIQMLEICIGFVPLMGVCYFTTARTLMCKMPNKRPRK 240  
 DB 181 NARCPIPFPRYIGTSMKALIQMLEICIGFVPLMGVCYFTTARTLMCKMPNKRPRK 240  
 QY 241 VLLTVIVIVITQLPNIVKFCRAIDIIISLTSCMSKRMIDIAOVETESIALFHSCLNP 300  
 DB 241 VLLTVIVIVITQLPNIVKFCRAIDIIISLTSCMSKRMIDIAOVETESIALFHSCLNP 300  
 QY 301 ILYVFMGASFKNYVMKAKKYSWRQROSVBEPDSEGPTEPTSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKAKKYSWRQROSVBEPDSEGPTEPTSTFSI 350

## RESULT 14

ADRO3495  
 ID ADRO3495 standard; protein; 378 AA.

AC ADRO3495;

XX 21-OCT-2004 (first entry)

XX Novel human cytokine receptor CCX CKR.

XX DE

XX XX

KW	antiallergic; antiinflammatory; antimicrobial; cytostatic;
KW	immunostimulant; immunosuppressive; CXK chemokine receptor; CCX CKR;
KW	EBI1-ligand chemokine; ELC; secondary lymphoid-tissue chemokine; SLC;
KW	thymus-expressed chemokine; TECK; chemokine binding activity;
KW	CCX CKR modulator; chemokine binding modulator; inflammation; allergy;
KW	autoimmune disease; graft rejection; cancer; infectious disease;
KW	immunosuppressive disease; human; receptor.
OS	Homo sapiens.
FH	Key Location/Qualifiers
FT	Misc-difference 350..352 /note= "Encoded by ATTTAAAGTAAAAC"
FT	Misc-difference 362..363 /note= "Encoded by GAATGATGC"
FT	Misc-difference 367..368 /note= "Encoded by AAATAAAC"
XX	US2004146926-A1.
PV	
PD	29-JUL-2004.
XX	
PP	24-FEB-2004; 2004US-0078701B.
PR	
PR	12-OCT-1999; 99US-0159015P.
PR	13-OCT-1999; 99US-0159210P.
PR	20-DEC-1999; 99US-0172979P.
PR	28-DEC-1999; 99US-0173388P.
PR	03-MAR-2000; 2000US-0186626P.
PR	10-OCT-2000; 2000US-0068601P.
PR	21-NOV-2000; 2000US-0072149S.
XX	
PA	(CHEM-) CHEMOCENTRYX INC.
PI	Gosling J, Dairgshi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
XX	
DR	WPI: 2004-561394/54.
XX	N-PSTDB; ADR03494.
PT	New CCX chemokine receptor polypeptide that binds ELC, SLC or TECK,
PT	useful in identifying modulators of its expression or activity which are
PT	potentially useful for treating inflammation, allergies, autoimmune
PT	disease and cancer.
XX	
PS	Claim 2, SEQ ID NO 2; 37pp; English.
XX	
CC	The invention describes an isolated or recombinant CCX chemokine receptor
CC	(CCX CKR) polypeptide (I) or its fragment that binds EBI1-ligand
CC	chemokine (ELC), Secondary lymphoid-tissue chemokine (SLC) or thymus-
CC	expressed chemokine (TECK). Also described are: a fusion protein
CC	comprising the polypeptide; an isolated polynucleotide encoding (I) or
CC	its fragment; an isolated polynucleotide comprising a sequence encoding a
CC	polypeptide that has a chemokine binding activity which is: a
CC	polynucleotide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:3; a
CC	polynucleotide that hybridises under stringent conditions to (a); or a
CC	polynucleotide sequence which is degenerate as a result of the genetic
CC	code to the sequences defined in (a) or (b); a recombinant (expression)
CC	vector comprising the polynucleotide; a host cell comprising the vector;
CC	producing a CCX CKR protein, peptide or fusion protein; a polynucleotide
CC	primer, probe, antisense oligonucleotide or ribozyme comprising at least
CC	15 contiguous bases identical or exactly complementary to the 1147-bp
CC	sequence; an antibody or its fragment that specifically binds to the
CC	polypeptide; an isolated cell capable of secreting the antibody; a
CC	hybridoma capable of secreting the antibody; detecting a CCX CKR gene
CC	product in a sample; amplifying a CCX CKR polynucleotide in a sample;
CC	identifying a modulator of the binding of CCX CKR to a chemokine;
CC	producing a pharmaceutical composition from a modulator of CCX CKR
CC	(chemokine binding) activity; identifying a modulator of CCX CKR activity
CC	; and treating a CCX CKR-mediated condition in a mammal. Agents that
CC	modulate the activity of CCX CKR in a cell or tissue in an animal are
CC	useful for treating CCX CKR related conditions such as inflammation,
CC	allergy, an autoimmune disease, graft rejection, cancer, an infectious
CC	disease or an immunosuppressive disease, preferably inflammation. This is

CC	the amino acid sequence of novel chemokine receptor CCX CKR.
XX	
SQ	Sequence 378 AA;
	Query Match 100.0%; Score 1819; DB 8; Length 378; Best Local Similarity 100.0%; Pred. No. 1.2e-194; Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MALRQNSTDYRYEENEMNGTYDYSQVHELICKEDVRFAVFLPVLTITVFVIGLAGNS 60   DB 1 MALEQNOSTDYRYEENEMNGTYDSQVELICKEDVRFAVFLPVLTITVFVIGLAGNS 60
OY	61 MVVAIYAYKKQRKRTDYIINLAVADLLLFTEPFMAVNAMHGVGKIMCKITSALYT 120   DB 61 MVVAIYAYKKQRKRTDYIINLAVADLLLFTEPFMAVNAMHGVGKIMCKITSALYT 120
OY	121 LNFVSQOPLACISIDRYAATKVPSOSGVGPCWIIICFCVMAAAILISTPOLVFTYND 180   DB 121 LNFVSQOPLACISIDRYAATKVPSOSGVGPCWIIICFCVMAAAILISTPOLVFTYND 180
OY	181 NARCIPIPRRLTGSMAKLIOMLRICGFVVFPILMGVCYFITTARTLMKMINKISRPLK 240   DB 181 NARCIPIPRRLTGSMAKLIOMLRICGFVVFPILMGVCYFITTARTLMKMINKISRPLK 240
OY	241 VLTFTVIVFIYTOLPYNIYVEKRAIDIYLSITSCNMSKRMDIAIQVTESIALPHSCLNP 300   DB 241 VLTFTVIVFIYTOLPYNIYVEKRAIDIYLSITSCNMSKRMDIAIQVTESIALPHSCLNP 300
OY	301 ILVYFMGASPKNYVMKAKKYGRRROQSVEEPDPSEGETPTSTFSI 350   DB 301 ILVYFMGASPKNYVMKAKKYGRRROQSVEEPDPSEGETPTSTFSI 350
RESULT 15	
ID	AAB62389 standard; protein; 382 AA.
XX	
AC	AAB62389;
DT	29-JUN-2001 (first entry)
XX	
DE	Human chemokine receptor CCX CKR polypeptide.
XX	
KW	Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator; antiflammatory; immunosuppressive; cyclostatic; antiallergic; human; immunostimulant; gene therapy.
KW	
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 351 /note= "encoded by TAA"
FT	Misc-difference 353 /note= "encoded by TAA"
FT	Misc-difference 365 /note= "encoded by TAA"
FT	Misc-difference 371 /note= "encoded by TGA"
FT	Misc-difference 371 /note= "encoded by TAA"
XX	
PN	WO200127146-A2.
PD	19-APR-2001.
XX	
PF	10-OCT-2000; 2000WO-US028067.
XX	
PR	12-OCT-1999; 99US-0159015P.
PR	13-OCT-1999; 99US-0159210P.
PR	20-DEC-1999; 99US-0172979P.
PR	28-DEC-1999; 99US-0173389P.
PR	03-MAR-2000; 2000US-0186626P.
XX	
PA	(CHEM-) CHEMOCENTRIX INC.
XX	

PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;  
 XX  
 DR WPI; 2001-281975/29.  
 DR N-PSDB; AAF57685.

XX Isolated or recombinant chemokine receptor (designated CCX CKR)  
 PT polypeptide (PI) or its fragment, useful for identifying CCX CKR  
 PT modulators which can be used in the treatment of inflammation, allergy,  
 PT an autoimmune disease or cancer.

XX Claim 4; Fig 1; 72p; English.

XX The invention relates to an isolated or recombinant chemokine receptor  
 CC designated CCX CKR) polypeptide which binds to chemokines such as ELC,  
 CC SLK or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR  
 CC modulators. An agent that modulates the activity or expression of CCX CKR  
 CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR  
 CC -mediated condition such as inflammation, allergy, an autoimmune disease,  
 CC graft rejection, cancer, an infectious disease or an immunosuppressive  
 CC disease. The present sequence represents the human CCX CKR polypeptide

XX Sequence 382 AA;

Query Match 100.0%; Score 1819; DB 4; Length 382;

Best Local Similarity 100.0%; Pred. No. 1.2e-194;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLEQNSTDYEEENENMGTYDYSEYELCIKEDVREFAKFLPVFLTIVFVIGLAGNS 60  
 DB 1 MLEQNSTDYEEENENMGTYDYSEYELCIKEDVREFAKFLPVFLTIVFVIGLAGNS 60  
 OY 61 MVAIAYKKKORTKTDVYTLNLAVALDLLFTLPFAVNAVHGWLGKIMCKITSAIYT 120  
 DB 61 MVAIAYKKKORTKTDVYTLNLAVALDLLFTLPFAVNAVHGWLGKIMCKITSAIYT 120  
 OY 121 LNFVSGMOFLACISIDRYAVATKVPQSGVGKPCWIIICFCVMAAILLSIPQLVFTYVND 180  
 DB 121 LNFVSGMOFLACISIDRYAVATKVPQSGVGKPCWIIICFCVMAAILLSIPQLVFTYVND 180  
 OY 181 NARCIPIPRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIIKISPLK 240  
 DB 181 NARCIPIPRYLGTSKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIIKISPLK 240  
 OY 241 VLTWTVIVFIVQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300  
 DB 241 VLTWTVIVFIVQLPYNIVKFCRAIDIIYSLITSCNMSKMDIAIQVTESIALFHSCLNP 300  
 OY 301 ILVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPTSTFSI 350  
 DB 301 ILVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPTSTFSI 350

Search completed: March 2, 2005, 04:21:34  
 Job time : 84 secs



Result No.	Score	Query Match	Length	DB	ID	Description
1	1819	100.0	350	9	US-09-765-994-2	Sequence 2, Appl1
2	1819	100.0	350	9	US-09-796-338A-8	Sequence 8, Appl1
3	1819	100.0	350	10	US-09-966-433-16	Sequence 16, Appl1
4	1819	100.0	350	14	US-10-288-837-8	Sequence 8, Appl1
5	1819	100.0	350	14	US-10-225-567A-607	Sequence 607, Appl1
6	1819	100.0	350	14	US-10-288-222A-10	Sequence 10, Appl1
7	1819	100.0	350	14	US-10-145-586-8	Sequence 8, Appl1
8	1819	100.0	350	14	US-10-233-423-75	Sequence 75, Appl1
9	1819	100.0	350	15	US-10-407-079-84	Sequence 84, Appl1
10	1819	99.7	339	9	US-09-765-994-4	Sequence 4, Appl1
11	1810	99.5	348	15	US-10-893-161-12	Sequence 12, Appl1
12	1810	99.5	350	10	US-09-876-076-22	Sequence 22, Appl1
13	1810	99.5	350	10	US-09-876-252-24	Sequence 24, Appl1

15	1810	99.5	350	14	US-10-372-983-.22	Sequence 22, Appl
14	1810	99.5	350	14	US-10-393-807-.22	Sequence 22, Appl
15	1810	99.5	350	15	US-10-414-8208-.24	Sequence 24, Appl
16	1810	99.5	350	16	US-10-723-955-.24	Sequence 24, Appl
17	1810	99.5	350	16	US-10-782-596-.22	Sequence 22, Appl
18	1810	99.5	350	16	US-09-810-695-.8	Sequence 8, Appl11
19	1803	99.1	350	10	US-09-568-413-.79	Sequence 79, Appl
20	1620	89.1	350	10	US-10-073-885-.74	Sequence 73, Appl
21	1257	69.1	242	14	US-10-376-774-1.1532	Sequence 153, Appl
22	862	47.4	164	15	US-09-764-893-.51	Sequence 91, Appl
23	761	41.8	175	9	US-09-764-886-.59	Sequence 59, Appl
24	761	41.8	175	9	US-09-764-886-.59	Sequence 59, Appl
25	761	41.8	175	9	US-09-764-886-.59	Sequence 59, Appl
26	761	41.8	175	10	US-09-764-886-.59	Sequence 59, Appl
27	761	41.8	175	10	US-09-764-886-.59	Sequence 59, Appl
28	761	41.8	175	11	US-09-764-875-.798	Sequence 79, Appl
29	761	41.8	175	11	US-10-073-865-.91	Sequence 91, Appl
30	761	41.8	175	14	US-10-1073-313-.382	Sequence 382, Appl
31	761	41.8	175	14	US-10-073-885-1.0	Sequence 100, Appl
32	659	36.2	378	14	US-10-251-385-.74	Sequence 74, Appl
33	659	36.2	378	14	US-10-251-5678-.68	Sequence 68, Appl
34	659	36.2	378	14	US-10-239-423-.70	Sequence 70, Appl
35	659	36.2	378	15	US-10-435-696-.48	Sequence 48, Appl
36	659	36.2	475	15	US-10-425-114-5.6811	Sequence 56811, Appl
37	655	36.0	378	14	US-10-551-385-.204	Sequence 204, Appl
38	643	35.3	369	14	US-10-239-423-.72	Sequence 72, Appl
39	643	35.3	378	9	US-09-939-5838-.2	Sequence 2, Appl1
40	643	35.3	378	14	US-10-164-646-4.9	Sequence 49, Appl
41	643	35.3	378	16	US-10-749-990-.2	Sequence 2, Appl1
42	637	35.0	357	9	US-09-903-377-.2	Sequence 2, Appl1
43	637	35.0	357	9	US-09-952-385-.2	Sequence 2, Appl1
44	637	35.0	357	10	US-09-866-755-.2	Sequence 2, Appl1
45	637	35.0	357	13	US-10-000-7559-.2	Sequence 2, Appl1

## ALIGNMENTS

```

RESULT 1
US-09-765-994-2
Sequence 2. Application US/09765994
Patent No. US2001001636A1
GENERAL INFORMATION:
APPLICANT: ELLIS, CATHERINE
TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
TITLE OF INVENTION: (HFT0A.1)
FILE REFERENCE: GH-70225-C1
CURRENT APPLICATION NUMBER: US/09/765,994
CURRENT FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/055,895
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: 08/962,922
PRIOR FILING DATE: 1997-10-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-765-994-2

```

Query Match	100.0%;	Score 1819;	DB 9;	Length 350;
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Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 M A L E Q N S T D Y Y E E N E M N G T Y D S Q Y E L I C I K E D V R E F A K V L P V F L T I V F I G L A G N S 60

1 MALEQNSTDYEEENENGTDYDYSQYELICIKEDVREFAKVELPVFLTIVFVIGLAGNS 60

61 M V V A I Y A Y K K R T K T D V Y I L N L A V A D L L L F T L P F W A V N A V H G W L G K I M C K I T S A L Y T 120

61 MVAIYAYKKQRTKTDVYILNLAVADLLLLFTLPFAVNVAHVGLKIMCKITSALYT 120

121 LNFVSGMQFLACISIDRYVAVTKVPSSQSGVGKPCWII CFCVWMAAILLSIPQLVFYTVND 180

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Db      121  LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICCVMAAIIILSIPQVFTYVND 180
      181  NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
      181  NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
      241  VLLTVIVIVTQLPNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
      241  VLLTVIVIVTQLPNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
      301  ILYVFMGASFKNYVMKVAKKYGSWRQROSVEEFPDSEGPTEPTSTFSI 350
      301  ILYVFMGASFKNYVMKVAKKYGSWRQROSVEEFPDSEGPTEPTSTFSI 350

```

```

RESULT 2
US-09-796-338A-8
; Sequence 8, Application US/09796338A
; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-338A-8

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Query Match      100.0%; Score 1819; DB 9; Length 350;
Best Local Similarity 100.0%; Pred. No. 9.7e-152;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MALLEONOSTDYEEENENANGTYDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNS 60
      1  MALLEONOSTDYEEENENANGTYDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNS 60
      61  MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
      61  MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
      121  LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICCVMAAIIILSIPQVFTYVND 180
      121  LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICCVMAAIIILSIPQVFTYVND 180
      181  NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
      181  NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
      241  VLLTVIVIVTQLPNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
      241  VLLTVIVIVTQLPNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
      301  ILYVFMGASFKNYVMKVAKKYGSWRQROSVEEFPDSEGPTEPTSTFSI 350
      301  ILYVFMGASFKNYVMKVAKKYGSWRQROSVEEFPDSEGPTEPTSTFSI 350

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RESULT 3
US-09-968-433-16
; Sequence 16, Application US/09968433
; Publication No. US20030073162A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Vanice

```

```

; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preeti
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PC-0051 CIP
; CURRENT APPLICATION NUMBER: US/09/968,433
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PERL Program
; SEQ ID NO 16
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073162A1 2547002CD1
US-09-968-433-16

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Query Match      100.0%; Score 1819; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 9.7e-152;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MALLEONOSTDYEEENENANGTYDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNS 60
      1  MALLEONOSTDYEEENENANGTYDYSQYELICIKEDVREFAKVFLPVFLTIIVFVIGLAGNS 60
      61  MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
      61  MVVAIYAYKKORTKTDVYILNLAVADLLFTLPFWAVNAVHGWVLGKIMCKITSALYT 120
      121  LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICCVMAAIIILSIPQVFTYVND 180
      121  LNFVSGMOFLACISIDRYAVATKVPSSQSGVKPCWIIICCVMAAIIILSIPQVFTYVND 180
      181  NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
      181  NARCIPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNIKISRPLK 240
      241  VLLTVIVIVTQLPNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
      241  VLLTVIVIVTQLPNIVKFCRAIDIIYSLITSCMSKRMIDAIQVTSIALFHSCLNP 300
      301  ILYVFMGASFKNYVMKVAKKYGSWRQROSVEEFPDSEGPTEPTSTFSI 350
      301  ILYVFMGASFKNYVMKVAKKYGSWRQROSVEEFPDSEGPTEPTSTFSI 350

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RESULT 4
US-10-282-837-8
; Sequence 8, Application US/10282837
; Publication No. US20030082738A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/10/282,837
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-837-8

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Query Match      100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 9.7e-152;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPVFLTVFVIGLAGNS 60  
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPVFLTVFVIGLAGNS 60  
 QY 61 MVVAIAAYKKORTKTVDYILNLAVADLLFLTPMAVNAVHGVLGIMCKITSALT 120  
 DB 61 MVVAIAAYKKORTKTVDYILNLAVADLLFLTPMAVNAVHGVLGIMCKITSALT 120  
 QY 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNIKISRPK 240  
 DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNIKISRPK 240  
 QY 241 VLLTVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300  
 DB 241 VLLTVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300  
 QY 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPSTFSI 350

## RESULT 5

US-10-225-567A-607  
 / Sequence 607, Application US/10225567A  
 / Publication No. US20030113798A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Lifespan Biosciences  
 / APPLICANT: Brown, Joseph F.  
 / APPLICANT: Burmer, Glenna C.  
 / APPLICANT: Roush, Christine L.  
 / TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 / FILE REFERENCE: 1920-4-4  
 / CURRENT APPLICATION NUMBER: US/10/225,567A  
 / PRIOR FILING DATE: 2001-12-19  
 / PRIOR APPLICATION NUMBER: 60/257,144  
 / NUMBER OF SEQ ID NOS: 2292  
 / SOFTWARE: PatentIn version 3.1  
 / SEQ ID NO 607  
 / LENGTH: 350  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / US-10-225-567A-607

Query Match 100.0%; Score 1819; DB 14; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-152;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPVFLTVFVIGLAGNS 60  
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPVFLTVFVIGLAGNS 60  
 QY 61 MVVAIAAYKKORTKTVDYILNLAVADLLFLTPMAVNAVHGVLGIMCKITSALT 120  
 DB 61 MVVAIAAYKKORTKTVDYILNLAVADLLFLTPMAVNAVHGVLGIMCKITSALT 120  
 QY 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNIKISRPK 240  
 DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNIKISRPK 240  
 QY 241 VLLTVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300  
 DB 241 VLLTVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300

QY 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPSTFSI 350

## RESULT 6

US-10-288-222A-10  
 / Sequence 10, Application US/10288222A  
 / Publication No. US20030119742A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Logan, Thomas Joseph  
 / APPLICANT: Galvin, Katherine  
 / APPLICANT: Chun, Mayoung  
 / TITLE OF INVENTION: Methods and Compositions to treat  
 / TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414,  
 / FILE REFERENCE: MP12001-286P1R(M)  
 / CURRENT APPLICATION NUMBER: US/10/288,222A  
 / PRIOR FILING DATE: 2002-11-05  
 / NUMBER OF SEQ ID NOS: 30  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 10  
 / LENGTH: 350  
 / TYPE: PRT  
 / ORGANISM: Homo sapien  
 / US-10-288-222A-10

Query Match 100.0%; Score 1819; DB 14; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-152;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPVFLTVFVIGLAGNS 60  
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVLPVFLTVFVIGLAGNS 60  
 QY 61 MVVAIAAYKKORTKTVDYILNLAVADLLFLTPMAVNAVHGVLGIMCKITSALT 120  
 DB 61 MVVAIAAYKKORTKTVDYILNLAVADLLFLTPMAVNAVHGVLGIMCKITSALT 120  
 QY 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 DB 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVKPCWIIICFCVMAAAILLSIPOLVFTYVND 180  
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNIKISRPK 240  
 DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNIKISRPK 240  
 QY 241 VLLTVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300  
 DB 241 VLLTVVIVFIVTQLPYNIIVKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300  
 QY 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPSTFSI 350  
 DB 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEGPTEPSTFSI 350

## RESULT 7

US-10-145-586-8  
 / Sequence 8, Application US/10145586  
 / Publication No. US20030138890A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Alexandra Gluckemann, Maria  
 / APPLICANT: Silos-Santiago, Immaculada  
 / APPLICANT: M. Galvin, Katherine  
 / APPLICANT: Welch, Nadine  
 / APPLICANT: Curtis, Roy A. J.  
 / APPLICANT: Bandaru, Rajasekhar  
 / APPLICANT: Kapeller-Libermann, Rosana  
 / TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,  
 / TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LECTIN-RICH  
 / FILE REFERENCE: 10448-188001  
 / CURRENT APPLICATION NUMBER: US/10/145,586



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?  
?   CURRENT FILING DATE: 2002-05-14  
? Prior Application removed - See File Wrapper or Palm  
? NUMBER OF SEO ID NOS: 95  
? SOFTWARE: PastSeq for Windows Version 4.0  
? SEO ID NO: 8  
? LENGTH: 350  
? TYPE: PRT  
? ORGANISM: Homo sapiens  
? OS-10-145-586-8
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Query Match	100.0%	Score 1819	DB 14	Length 350
Best Local Similarity	100.0%	Pred. No. 9.7e-152		
Matches 350; Conservative	0	Mismatches	0	Gaps 0

QY	1	MALENOGSDYXXEENENNGTADYSQYELICIEDVREBAKFLPAFLTLVFIYGLAGNS	60
Db	1	MALENOGSDYXXEENENNGTADYSQYELICIEDVREBAKFLPAFLTLVFIYGLAGNS	60
QY			
Db	61	MVVAIYAYKKRRTDVTYIILMAVADLLPLPMAVANAHVGLKIMCITSALYT	120
QY			
Db	61	MVVAIYAYKKRRTDVTYIILMAVADLLPLPMAVANAHVGLKIMCITSALYT	120
QY	121	INFVSGMOFLACISIDRYVAATVKSBSQSGVGKRCWICFCVMAAAILLSIPOLVFYVND	180
Db	121	INFVSGMOFLACISIDRYVAATVKSBSQSGVGKRCWICFCVMAAAILLSIPOLVFYVND	180
QY			
Db	181	NARCIPIPRXYIGTSMKALIQMLETICIGVVPPLINGVCYFIFTARTLMKPNKIKISPLK	240
QY			
Db	181	NARCIPIPRXYIGTSMKALIQMLETICIGVVPPLINGVCYFIFTARTLMKPNKIKISPLK	240
QY	241	VLLTVVIVFIYVLOLPINIVKFCRAIDIIYSLITSCKMSKMDIAIQVTESIALFHSCLNP	300
Db	241	VLLTVVIVFIYVLOLPINIVKFCRAIDIIYSLITSCKMSKMDIAIQVTESIALFHSCLNP	300
QY	301	ILYVMGASFKNYVMKVAKKYSGMROROSVEEPFDSRCPETSTFSI	350
Db	301	ILYVMGASFKNYVMKVAKKYSGMROROSVEEPFDSRCPETSTFSI	350

RESULT 8  
US-10-239-423-75

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Publication NO. US20030186889A1
GENERAL INFORMATION:
APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERWANN, Knut;
APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
FILE REFERENCE: 022217us
CURRENT APPLICATION NUMBER: US/10/239,423
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: DE10016013.1
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 75
LENGTH: 350
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-75

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Query Match	100.0%;	Score 1819;	DB 14;	Length 350;
Best Local Similarity	100.0%;	Pred. NO. 9.7e-152;		
Matches 350;	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MALEQNSTDYEENEMNGTYDSQYELICIKEDVREFAKVFLPVFLTIVFVIGNS 600

Db 1 MALEQNSTDYEEENMGTYDYSQYELICKEDVREFAKVPLPVFLTIVFVIGLAGNS 60

61 MVAIYAYKKQRTKDVILNLAVADLLLFTLPFAVNVAHVGLGKIMCKITSALYT 120

Db 61 M VVA IY A Y Y K Q R T K T D V Y I L N L A V A D L L L F T L P F W A V N A V H G W L G K I M C K I T S A L Y T 120

121 LNFVSGMQFLACISIDRYAVTKVPSQSGVGKPCWILCFQVWMAALLSLPQLVFYVND 180

DB 121 LNFVSGMQLPACISIDRIVAHINAVPSQSGVGNCMLICFCVMZKAIJESIFQDVEIYAND 100

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[illegible]

Db 341 Wt TWTVEITOTI PVNTVKECPBAIDITYSI.ITSCNMSKBPMDIAIOVTESIAL.EHSCTJ.NP 300

301 ILVYFMGASPKNYMKVAKKYGSWRBOROSVEEPPDSEGPTEPTSTFSI 350

Db 301 ILVFMGASFKNYVMKVAKKYGSWRQRQSVVEFPFDSEGTEPTSTFSI 350

; Sequence 84, Application US/10407079  
; Publication No. US20030215860A1

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Query Match	100.0%	Score 1819;	DB 15;	Length 350;
Best Local Similarity	100.0%;	Pred. No. 9,7e-152;		
Matches 350, Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 M A L E Q N O S T D Y Y E E N E M N G T Y D S Q Y E L I C I K E D V R E F A K V L P V F L T I V F I G L A G N S 60

Db 1 MLEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
 Qy 61 MVAIYAYKKORTKTDVYILNLAVADLLFTLPFMANVAHGWVLGKIMCKITSALT 120  
 Db 61 MVAIYAYKKORTKTDVYILNLAVADLLFTLPFMANVAHGWVLGKIMCKITSALT 120  
 Qy 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILSIPLQVFTYVND 180  
 Db 121 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILSIPLQVFTYVND 180  
 Qy 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240  
 Db 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240  
 Qy 241 VLTAVIVFIVTQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIQVTESTIALFHSCLNP 300  
 Db 241 VLTAVIVFIVTQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIQVTESTIALFHSCLNP 300  
 Qy 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEPTSTFSI 350  
 Db 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEPTSTFSI 350

# RESULT 10 US-09-765-994-4

; Sequence 4, Application US/09765994  
 ; Patent No. US20010016336A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELLIS, CATHERINE  
 ; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR  
 ; FILE REFERENCE: GH-70225-CI  
 ; CURRENT APPLICATION NUMBER: US/09/765,994  
 ; CURRENT FILING DATE: 2001-01-19  
 ; PRIOR APPLICATION NUMBER: 60/055,895  
 ; PRIOR FILING DATE: 1997-08-15  
 ; PRIOR APPLICATION NUMBER: 08/962,922  
 ; PRIOR FILING DATE: 1997-10-27  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FaSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: HOMO SAPIENS  
 US-09-765-994-4

Query Match 99.7%; Score 1814; DB 9; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-151;  
 Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 61  
 Db 1 ALEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
 Qy 62 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFMANVAHGWVLGKIMCKITSALT 121  
 Db 61 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFMANVAHGWVLGKIMCKITSALT 120  
 Qy 122 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILSIPLQVFTYVND 181  
 Db 122 INFVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILSIPLQVFTYVND 180  
 Qy 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 241  
 Db 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240  
 Qy 242 LTVAVIVFIVTQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIQVTESTIALFHSCLNP 301  
 Db 241 LTVAVIVFIVTQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIQVTESTIALFHSCLNP 300  
 Qy 302 LYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEPTSTFSI 350  
 Db 301 LYVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEPTSTFSI 349

RESULT 11  
 US-10-403-161-12  
 ; Sequence 12, Application US/10403161  
 ; Publication No. US20040043930A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, David et al.  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-573C  
 ; CURRENT APPLICATION NUMBER: US/10/403,161  
 ; CURRENT FILING DATE: 2003-03-31  
 ; PRIOR APPLICATION NUMBER: 60/370349  
 ; PRIOR FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: 60/384543  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: 60/370969  
 ; PRIOR FILING DATE: 2002-04-08  
 ; PRIOR APPLICATION NUMBER: 60/403748  
 ; PRIOR FILING DATE: 2002-08-15  
 ; PRIOR APPLICATION NUMBER: 60/372019  
 ; PRIOR FILING DATE: 2002-04-12  
 ; PRIOR APPLICATION NUMBER: 60/374379  
 ; PRIOR FILING DATE: 2002-04-22  
 ; PRIOR APPLICATION NUMBER: 09/779679  
 ; PRIOR FILING DATE: 2001-02-08  
 ; PRIOR APPLICATION NUMBER: 60/181045  
 ; PRIOR FILING DATE: 2000-02-08  
 ; PRIOR APPLICATION NUMBER: 10/055877  
 ; PRIOR FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: 60/262892  
 ; Remaining Prior Application data removed - See file wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 173  
 ; SOFTWARE: CuroSeqList version 0.1  
 ; SEQ ID NO 12  
 ; LENGTH: 348  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-403-161-12

Query Match 99.5%; Score 1810; DB 15; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 6e-151;  
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 62  
 Db 1 LEQNSTDYEEENMGTYDSQYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
 Qy 63 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFMANVAHGWVLGKIMCKITSALT 122  
 Db 61 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFMANVAHGWVLGKIMCKITSALT 120  
 Qy 123 FVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILSIPLQVFTYVND 182  
 Db 121 FVSGMOPLACISIDRYAVATKVPSSQGVGKPCWIIICFCVMAAIIILSIPLQVFTYVND 180  
 Qy 183 RCIPPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 242  
 Db 181 RCIPPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240  
 Qy 243 LTVAVIVFIVTQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIQVTESTIALFHSCLNP 302  
 Db 241 LTVAVIVFIVTQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIQVTESTIALFHSCLNP 300  
 Qy 303 YVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEPTSTFSI 350  
 Db 301 YVFMGASFKNYVMKAKKYGSMRQROSVBEFPDSEPTSTFSI 348

RESULT 12  
 US-09-875-076-22  
 ; Sequence 22, Application US/09875076

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/ Publication No. US20030017528A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/09/875,076
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,293
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 350
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-875-076-22

Query Match          99.5%; Score 1810; DB 10; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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121 INFVSGMOFLACISIDRYVAATNVPQSOSGVGKPCWIIICFVMAAILISIPQLVFYTVND 180
181 NARCIPIPRYIGTSMKLLIOMLEICIGFVVPFLMGVCYFTATTLMKMPRIKSRPK 240
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241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSILTSQMSKMDIAIQVTESIALFHSCLNP 300
241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSILTSQMSKMDIAIQVTESIALFHSCLNP 300
301 ILVFMGASFKNYVMKVAKKYGSWROROSVEEFPDSBGPTEPTSTSI 350
301 ILVFMGASFKNYVMKVAKKYGSWROROSVEEFPDSBGPTEPTSTSI 350

RESULT 13
US-09-876-252-24
/ Sequence 24, Application US/09876252
/ Publication No. US20030018182A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Lehmann-Brinema, Karin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Rec
/ FILE REFERENCE: AREN-0054
/ CURRENT APPLICATION NUMBER: US/09/876,252
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/152,524
/ PRIOR FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: 60/151,114
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
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/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
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/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ NUMBER OF SEQ ID NOS: 146
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 24
/ LENGTH: 350
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-876-252-24
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Query Match          99.5%; Score 1810; DB 10; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 1 MLEQNOSTDYEEENENNGTYDYSQYELICKEDEVEPAKYFLPVFLTIIVFVIGLAGNS 60
QY 61 MVAIYAAYKKORTKTIDYIILMAVADLLFLPLPMAVNAVHGWLGKIMCKITSALYT 120
DB 61 MVAIYAAYKKORTKTIDYIILMAVADLLFLPLPMAVNAVHGWLGKIMCKITSALYT 120
QY 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
DB 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIKISRPLK 240
DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIKISRPLK 240
QY 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300
DB 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300
QY 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350
DB 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350
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## RESULT 14

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US-10-272-983-22
/ Sequence 22, Application US/10272983
/ Publication No. US20030148450A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/10/272,983
/ PRIOR FILING DATE: 2002-10-17
/ PRIOR APPLICATION NUMBER: US/09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/109,213
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/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 350
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-272-983-22
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Query Match          99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 MLEQNOSTDYEEENENNGTYDYSQYELICKEDEVEPAKYFLPVFLTIIVFVIGLAGNS 60
DB 1 MLEQNOSTDYEEENENNGTYDYSQYELICKEDEVEPAKYFLPVFLTIIVFVIGLAGNS 60
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DB 61 MVAIYAAYKKORTKTIDYIILMAVADLLFLPLPMAVNAVHGWLGKIMCKITSALYT 120
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DB 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICVMAAAILLSIPOLVFYTVND 180
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DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVFPFLMGVCYFTTARTLMKMPNIKISRPLK 240
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DB 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAIQVTSIALFHSCLNP 300
QY 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350
DB 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350
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## RESULT 15

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US-10-393-807-22
/ Sequence 22, Application US/10393807
/ Publication No. US20030175891A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/10/393,807
/ PRIOR FILING DATE: 2003-03-21
/ PRIOR APPLICATION NUMBER: US/09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/120,416
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/ PRIOR FILING DATE: 1999-02-16  
/ PRIOR APPLICATION NUMBER: 60/121, 851  
/ PRIOR FILING DATE: 1999-02-26  
/ PRIOR APPLICATION NUMBER: 60/123, 946  
/ PRIOR FILING DATE: 1999-03-12  
/ PRIOR APPLICATION NUMBER: 60/123, 949  
/ PRIOR FILING DATE: 1999-03-12  
/ PRIOR APPLICATION NUMBER: 60/136, 436  
/ PRIOR FILING DATE: 1999-05-28  
/ PRIOR APPLICATION NUMBER: 60/136, 437  
/ PRIOR FILING DATE: 1999-05-28  
/ PRIOR APPLICATION NUMBER: 60/136, 439  
/ PRIOR FILING DATE: 1999-05-28  
/ PRIOR APPLICATION NUMBER: 60/136, 567  
/ PRIOR FILING DATE: 1999-05-28  
/ Remaining Prior Application data removed - See File Wrapper or PALM.  
/ NUMBER OF SEQ ID NOS: 74  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 22  
/ LENGTH: 350  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-10-393-807-22

Query Match 99.5%; Score 1810; DB 14; Length 350;  
Best Local Similarity 99.4%; Pred. No. 6e-151;  
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLEONQSTDYEEENMGCTYDYSOYELICTKEDVREFAKVPVFLTVFVIGLAGNS 60  
DB 1 MLEONQSTDYEEENMGCTYDYSOYELICTKEDVREFAKVPVFLTVFVIGLAGNS 60  
QY 61 MVAIAIYAYKKORTKTDVYIILNLA VADLLFLTPFMAVNAVHGWVLGKIMCKITSALYT 120  
DB 61 MVAIAIYAYKKORTKTDVYIILNLA VADLLFLTPFMAVNAVHGWVLGKIMCKITSALYT 120  
QY 121 INFVSGMOFLACISIDRYVAATKVPSSQSVGKPCWIIICFCWMAAILLSIPQLVFTYVND 180  
DB 121 INFVSGMOFLACISIDRYVAATKVPSSQSVGKPCWIIICFCWMAAILLSIPQLVFTYVND 180  
QY 181 NARCTPIPRRYLGTSMKALIQMLEICIGFVVPPLIMGVCYFTARTLMKMPNIKISRPLK 240  
DB 181 NARCTPIPRRYLGTSMKALIQMLEICIGFVVPPLIMGVCYFTARTLMKMPNIKISRPLK 240  
QY 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITS CNMSKRMDAIQVTSIALFHSCLNP 300  
DB 241 VLLTVIVIVITQLPYNIVKFCRAIDIIYSLITS CNMSKRMDAIQVTSIALFHSCLNP 300  
QY 301 ILYVFMGASFKNYVMKVAKKYGSWRROSVBEFPDSEGPTEPTSTFSI 350  
DB 301 ILYVFMGASFKNYVMKVAKKYGSWRROSVBEFPDSEGPTEPTSTFSI 350

Search completed: March 2, 2005, 04:34:39  
Job time : 137 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:18:17 ; Search time 22 Seconds  
(without alignments)  
1187.599 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819

Sequence: 1 MALBQNSQSDYYEENEMNG.....VEFPDSEGTPTPTSTFST 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/prodata/1/iaa/6CTUS\_COMB.pep:\*
- 6: /cgn2\_6/prodata/1/iaa/backfile1.pep:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16 Sequence 16, Appl
2	1819	100.0	350	4	US-09-721-908-2 Sequence 2, Appl
3	1819	100.0	350	4	US-09-721-341-2 Sequence 2, Appl
4	1819	100.0	350	4	US-09-721-495B-2 Sequence 2, Appl
5	1808	99.4	350	4	US-09-556-002-2 Sequence 2, Appl
6	1803	99.1	350	4	US-09-910-695-8 Sequence 8, Appl
7	1620	89.1	350	2	US-08-966-316-18 Sequence 18, Appl
8	659	36.2	358	3	US-08-153-848-19 Sequence 19, Appl
9	659	36.2	358	3	US-09-299-843A-19 Sequence 19, Appl
10	659	36.2	358	3	US-09-088-337B-19 Sequence 19, Appl
11	659	36.2	358	5	PCT-US93-11153-19 Sequence 19, Appl
12	659	36.2	378	1	US-08-153-848-15 Sequence 15, Appl
13	659	36.2	378	3	US-09-299-843A-15 Sequence 15, Appl
14	659	36.2	378	3	US-09-251-545-1 Sequence 1, Appl
15	659	36.2	378	3	US-09-088-337B-15 Sequence 15, Appl
16	659	36.2	378	4	US-09-170-496D-74 Sequence 74, Appl
17	659	36.2	378	5	PCT-US93-11153-15 Sequence 15, Appl
18	659	36.2	410	1	US-08-153-848-7 Sequence 7, Appl
19	659	36.2	410	3	US-09-299-843A-7 Sequence 7, Appl
20	659	36.2	410	3	US-09-088-337B-7 Sequence 7, Appl
21	659	36.2	410	5	PCT-US93-11153-7 Sequence 7, Appl
22	655	36.0	378	4	US-09-170-496D-204 Sequence 204, App
23	650	35.7	378	3	US-09-299-843A-66 Sequence 66, Appl
24	650	35.7	378	3	US-09-088-337B-66 Sequence 66, Appl
25	643	35.3	369	4	US-09-721-341-6 Sequence 6, Appl
26	643	35.3	369	4	US-09-721-495B-6 Sequence 6, Appl
27	643	35.3	371	4	US-09-949-016-11223 Sequence 11223, A

28	643	35.3	378	1	US-08-383-750-2 Sequence 2, Appl
29	643	35.3	378	1	US-08-383-751A-2 Sequence 2, Appl
30	643	35.3	378	3	US-08-352-678-2 Sequence 2, Appl
31	643	35.3	378	3	US-09-045-583-49 Sequence 49, Appl
32	643	35.3	378	4	US-09-534-185-49 Sequence 49, Appl
33	643	35.3	378	4	US-09-536-954-2 Sequence 2, Appl
34	643	35.3	378	4	US-09-929-583B-2 Sequence 2, Appl
35	643	35.3	378	4	US-09-721-341-7 Sequence 7, Appl
36	643	35.3	378	5	PCT-US93-09636-2 Sequence 2, Appl
37	643	35.3	378	5	PCT-US93-09636-2 Sequence 2, Appl
38	637	35.0	357	3	US-09-266-464-2 Sequence 2, Appl
39	637	35.0	357	4	US-09-170-496D-24 Sequence 24, Appl
40	637	35.0	357	4	US-09-952-385-2 Sequence 2, Appl
41	637	35.0	369	4	US-08-826-509-481 Sequence 481, App
42	635.5	34.9	359	1	US-08-153-848-24 Sequence 24, Appl
43	635.5	34.9	359	3	US-09-299-843A-24 Sequence 24, Appl
44	635.5	34.9	359	3	US-09-088-337B-24 Sequence 24, Appl
45	635.5	34.9	359	5	PCT-US93-11153-24 Sequence 24, Appl

## ALIGNMENTS

RESULT 1  
US-08-966-316-16  
; Sequence 16, Application US/08966316  
; Patent No. 5932445  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Reddy, Roopa  
; APPLICANT: Murty, Lynn B.  
; APPLICANT: Mathur, Preeti  
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/966,316  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0424 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: UTRSN0T11  
; CLONE: 2547002  
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.6e-148;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEBONOSTDYEEENBNNGTYDYSOYELICIKEDREPAKFLPFLITIVFVIGLAGNS 60  
DB 1 MLEBONOSTDYEEENBNNGTYDYSOYELICIKEDREPAKFLPFLITIVFVIGLAGNS 60  
QY 61 MVAIAYAYKKORTKTDVYIILNLAVADLLFLTPFMAVNAVHGVNLGKIMCKITSAIYT 120  
DB 61 MVAIAYAYKKORTKTDVYIILNLAVADLLFLTPFMAVNAVHGVNLGKIMCKITSAIYT 120  
QY 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICFCVMAAIIILSIPOLVFYTVND 180  
DB 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICFCVMAAIIILSIPOLVFYTVND 180  
QY 181 NARCIPIPRRYIGTSMKALIQMLEICIGVVPFLMGVCYFTTARTLMKMPINKISRPK 240  
DB 181 NARCIPIPRRYIGTSMKALIQMLEICIGVVPFLMGVCYFTTARTLMKMPINKISRPK 240  
QY 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300  
DB 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300  
QY 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVVEEPPDSEGPTEPTSTFSI 350  
DB 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVVEEPPDSEGPTEPTSTFSI 350

RESULT 2  
US-09-721-908-2  
Sequence 2, Application US/09721908  
Patent No. 6699677  
GENERAL INFORMATION:  
APPLICANT: Schall, Thomas J.  
APPLICANT: Tailbot, Dale  
APPLICANT: Zhenhua, Miao  
APPLICANT: Zheng, Wei  
APPLICANT: Chemocentrx, Inc.  
TITLE OF INVENTION: Tethered Ligands and Methods of Use  
FILE REFERENCE: 019934-001210US  
CURRENT APPLICATION NUMBER: US/09/721,908  
PRIOR FILING DATE: 2000-11-24  
PRIOR APPLICATION NUMBER: US 60/186,626  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 103  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Homo sapiens  
OTHER INFORMATION: human CCR10  
US-09-721-908-2

Query Match 100.0%; Score 1819; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.6e-148;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEBONOSTDYEEENBNNGTYDYSOYELICIKEDREPAKFLPFLITIVFVIGLAGNS 60  
DB 1 MLEBONOSTDYEEENBNNGTYDYSOYELICIKEDREPAKFLPFLITIVFVIGLAGNS 60  
QY 61 MVAIAYAYKKORTKTDVYIILNLAVADLLFLTPFMAVNAVHGVNLGKIMCKITSAIYT 120  
DB 61 MVAIAYAYKKORTKTDVYIILNLAVADLLFLTPFMAVNAVHGVNLGKIMCKITSAIYT 120  
QY 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICFCVMAAIIILSIPOLVFYTVND 180  
DB 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICFCVMAAIIILSIPOLVFYTVND 180  
QY 181 NARCIPIPRRYIGTSMKALIQMLEICIGVVPFLMGVCYFTTARTLMKMPINKISRPK 240  
DB 181 NARCIPIPRRYIGTSMKALIQMLEICIGVVPFLMGVCYFTTARTLMKMPINKISRPK 240

QY 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300  
DB 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300  
QY 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVVEEPPDSEGPTEPTSTFSI 350  
DB 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVVEEPPDSEGPTEPTSTFSI 350

RESULT 3  
US-09-721-341-2  
Sequence 2, Application US/09721341  
Patent No. 6828108  
GENERAL INFORMATION:  
APPLICANT: Gosling, Jennifa  
APPLICANT: Dairaghi, Daniel J.  
APPLICANT: Hanley, Michael  
APPLICANT: Miao, Zhenhua  
APPLICANT: Schall, Thomas J.  
APPLICANT: Chemocentrx, Inc.  
TITLE OF INVENTION: Chemokine Receptor  
FILE REFERENCE: 019934-000710US  
CURRENT APPLICATION NUMBER: US/09/721,341  
PRIOR FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: US 09/686,020  
PRIOR FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/159,015  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: US 60/159,210  
PRIOR FILING DATE: 1999-10-13  
PRIOR APPLICATION NUMBER: US 60/172,979  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: US 60/173,388  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: US 60/186,626  
PRIOR FILING DATE: 2000-03-03  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: chemokine receptor (CXK CCR)  
US-09-721-341-2

Query Match 100.0%; Score 1819; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.6e-148;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEBONOSTDYEEENBNNGTYDYSOYELICIKEDREPAKFLPFLITIVFVIGLAGNS 60  
DB 1 MLEBONOSTDYEEENBNNGTYDYSOYELICIKEDREPAKFLPFLITIVFVIGLAGNS 60  
QY 61 MVAIAYAYKKORTKTDVYIILNLAVADLLFLTPFMAVNAVHGVNLGKIMCKITSAIYT 120  
DB 61 MVAIAYAYKKORTKTDVYIILNLAVADLLFLTPFMAVNAVHGVNLGKIMCKITSAIYT 120  
QY 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICFCVMAAIIILSIPOLVFYTVND 180  
DB 121 INFVSGMOFLACISIDRYAAVTKVPSQSGVGKPCWIIICFCVMAAIIILSIPOLVFYTVND 180  
QY 181 NARCIPIPRRYIGTSMKALIQMLEICIGVVPFLMGVCYFTTARTLMKMPINKISRPK 240  
DB 181 NARCIPIPRRYIGTSMKALIQMLEICIGVVPFLMGVCYFTTARTLMKMPINKISRPK 240  
QY 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300  
DB 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300  
QY 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVVEEPPDSEGPTEPTSTFSI 350  
DB 301 ILYVFMGASFKNYVMKAKKYGSMRQROSVVEEPPDSEGPTEPTSTFSI 350



Db 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350

RESULT 4  
US-09-721-495B-2  
Sequence 2, Application US/09721495B  
Patent No. 6835547  
GENERAL INFORMATION:  
APPLICANT: Gossling, Jennife  
APPLICANT: Dairaghi, Daniel J.  
APPLICANT: Hanley, Michael  
APPLICANT: Miao, Zhenhua  
APPLICANT: Talbot, Dale  
APPLICANT: Schall, Thomas J.  
APPLICANT: Chemocentrx, Inc.  
TITLE OF INVENTION: Chemokine Receptor  
FILE REFERENCE: 019934-0007210US  
CURRENT APPLICATION NUMBER: US/09/721,495B  
CURRENT FILING DATE: 2000-11-21  
PRIOR APPLICATION NUMBER: US 60/159,015  
PRIOR FILING DATE: 1999-10-12  
PRIOR APPLICATION NUMBER: US 60/159,210  
PRIOR FILING DATE: 1999-10-13  
PRIOR APPLICATION NUMBER: US 60/172,979  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: US 60/173,388  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: US 60/186,626  
PRIOR FILING DATE: 2000-03-03  
PRIOR APPLICATION NUMBER: US 09/686,019  
PRIOR FILING DATE: 2000-10-10  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: chemokine receptor CCX CKR  
US-09-721-495B-2

Query Match 100.0%; Score 1819; DB 4; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1,6e-148;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLTIVFVIGLAGNS 60  
| | | | |  
Db 1 MALEQNSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLTIVFVIGLAGNS 60  
| | | | |  
QY 61 MVAIAYKKKQRTKTDVYILMLAVADLLFTLPFWANAVHGWLGKIMKITSALYT 120  
| | | | |  
Db 61 MVAIAYKKKQRTKTDVYILMLAVADLLFTLPFWANAVHGWLGKIMKITSALYT 120  
| | | | |  
QY 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAIIILSIPOLVFTYND 180  
| | | | |  
Db 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAIIILSIPOLVFTYND 180  
| | | | |  
QY 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAIIILSIPOLVFTYND 180  
| | | | |  
Db 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAIIILSIPOLVFTYND 180  
| | | | |  
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRPK 240  
| | | | |  
Db 181 NARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRPK 240  
| | | | |  
QY 241 VLLTVIVIVTQLPNIVKFCRAIDIIYSLTSCMSKRMIDAIQVTSIALFHSCLNP 300  
| | | | |  
Db 241 VLLTVIVIVTQLPNIVKFCRAIDIIYSLTSCMSKRMIDAIQVTSIALFHSCLNP 300  
| | | | |  
QY 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350  
| | | | |  
Db 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350  
| | | | |

Patent No. 6620615  
GENERAL INFORMATION:  
APPLICANT: Gould-Rothberg, Bonnie  
APPLICANT: Curagen Corporation  
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR AND METHOD OF USING SAME  
FILE REFERENCE: 15966-550  
CURRENT APPLICATION NUMBER: US/09/556,002  
CURRENT FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: USSN 60/130,817  
PRIOR FILING DATE: 1999-04-23  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-556-002-2

Query Match 99.4%; Score 1808; DB 4; Length 350;  
Best Local Similarity 99.4%; Pred. No. 1,4e-147;  
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLTIVFVIGLAGNS 60  
| | | | |  
Db 1 MALEQNSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLTIVFVIGLAGNS 60  
| | | | |  
QY 61 MVAIAYKKKQRTKTDVYILMLAVADLLFTLPFWANAVHGWLGKIMKITSALYT 120  
| | | | |  
Db 61 MVAIAYKKKQRTKTDVYILMLAVADLLFTLPFWANAVHGWLGKIMKITSALYT 120  
| | | | |  
QY 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAIIILSIPOLVFTYND 180  
| | | | |  
Db 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAIIILSIPOLVFTYND 180  
| | | | |  
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRPK 240  
| | | | |  
Db 181 NARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRPK 240  
| | | | |  
QY 241 VLLTVIVIVTQLPNIVKFCRAIDIIYSLTSCMSKRMIDAIQVTSIALFHSCLNP 300  
| | | | |  
Db 241 VLLTVIVIVTQLPNIVKFCRAIDIIYSLTSCMSKRMIDAIQVTSIALFHSCLNP 300  
| | | | |  
QY 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350  
| | | | |  
Db 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350  
| | | | |

RESULT 6  
US-09-910-695-8  
Sequence 8, Application US/09910695  
Patent No. 6737252  
GENERAL INFORMATION:  
APPLICANT: Hedrick, Joseph A.  
APPLICANT: Vicari, Alain P.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Mammalian Chemokines; Receptors;  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSER: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/910,695  
FILING DATE: 20-Jul-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/122,585  
FILING DATE: 24-JUL-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX0757  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 852-9196  
TELEFAX: (650) 496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-910-695-8

Query Match 99.1%; Score 1803; DB 4; Length 350;  
Best Local Similarity 99.4%; Pred. No. 3.8e-147;  
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALLEONQSTDYEEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
DB 1 MALLEONQSTDYEEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
QY 61 MVAIAIYAYKKRTKTDVYILNLAVADLLFLTPMVAANAAGVWGKIMKITSALT 120  
DB 61 MVAIAIYAYKKRTKTDVYILNLAVADLLFLTPMVAANAAGVWGKIMKITSALT 120  
QY 121 LNFVSGMOPFLACISIDRYAVATKVPSSQSGVKPCWIIICFVMAAIIISIPOLVFYTVND 180  
DB 121 LNFVSGMOPFLACISIDRYAVATKVPSSQSGVKPCWIIICFVMAAIIISIPOLVFYTVND 180  
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVPLINGVCYFIPTARTLMKMPNIIKISRLK 240  
DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVPLINGVCYFIPTARTLMKMPNIIKISRLK 240  
QY 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300  
DB 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300  
QY 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGPTEPTSTFSI 350  
DB 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

## RESULT 7

US-08-966-316-18  
Sequence 18, Application US/08966316  
Patent No. 5932445  
GENERAL INFORMATION:  
APPLICANT: Lal, Preeti  
APPLICANT: Au-Young, Janice  
APPLICANT: Reddy, Roopa  
APPLICANT: Murthy, Lynn E.  
APPLICANT: Mathur, Preete  
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/966,316  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0424 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 397711  
US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;  
Best Local Similarity 86.0%; Pred. No. 2e-131;  
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALLEONQSTDYEEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
DB 1 MALLEONQSTDYEEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60  
QY 61 MVAIAIYAYKKRTKTDVYILNLAVADLLFLTPMVAANAAGVWGKIMKITSALT 120  
DB 61 MVAIAIYAYKKRTKTDVYILNLAVADLLFLTPMVAANAAGVWGKIMKITSALT 120  
QY 121 LNFVSGMOPFLACISIDRYAVATKVPSSQSGVKPCWIIICFVMAAIIISIPOLVFYTVND 180  
DB 121 LNFVSGMOPFLACISIDRYAVATKVPSSQSGVKPCWIIICFVMAAIIISIPOLVFYTVND 180  
QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVPLINGVCYFIPTARTLMKMPNIIKISRLK 240  
DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVPLINGVCYFIPTARTLMKMPNIIKISRLK 240  
QY 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300  
DB 241 VLLTVIVIVITQLPNIYKFCRAIDIIYSLITSCNMSKRMDAIOVTESIALFHSCLNP 300  
QY 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGPTEPTSTFSI 350  
DB 301 ILVFMGASFKNYVMKAKYGSWROROSVEEFPDSEGPTEPTSTFSI 350

## RESULT 8

US-08-153-848-19  
Sequence 19, Application US/08153848  
Patent No. 5759804  
GENERAL INFORMATION:  
APPLICANT: Godiska, Ronald  
APPLICANT: Gray, Patrick W.  
APPLICANT: Schweikart, Vicki L.  
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,848  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5759804and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31794  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-153-848-19

Query Match 36.2%; Score 659; DB 1; Length 358;  
Best Local Similarity 38.7%; Pred. No. 7e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONQSTDYEEENMGNTYDYSOYELICIKEDYREPAKVPFLPFLITVIVIGLAGNS 60  
DB 1 VCLCODEVTDDYIDGNT--TVDYTLFESLCSKDVNRKAWFLPTMYSIICFVGLGNG 57  
QY 61 MVVAIYAYYKORTKTVDYILNLAADVADLLFTLPMAVNAVHGVGLGIMCKITSALYT 120  
DB 58 LVVLTYYIKRLKMTDYLNLAVADILFLTLTPMAVSAKSWFGVHFCGLIPAIYK 117  
QY 121 LNFVSGMQLACISIDRYAVATKVP--QSGVGKPCWIIICVWMAAILSLIPOLVY 176  
DB 118 MSFSGMMLLLCISIDRYAVAIQAVSAHRHRAVLLISKSCVGIWILATVISIPELVS 177  
QY 177 TVNDNA-----RCIPFPRLYLGTSKALIQMEICIGFVVPPLINGVCFTIARTLMKP 231  
DB 178 DLORSSSEQAMRCSLITTEH---VEAFITIOVQMWIGFVPLPAMSFCVLVIIRTLQAR 234  
QY 232 NIKISRPLKVLTVVIFVITQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIOVTEST 291  
DB 235 NEBRKAIVITAVVVFIVFQLPYNGVLAQTVANFNITSSITCSELKOLNIAVDYTSI 294  
QY 292 ALFHSGLNLDILYVFMGASPKYVMVAKKYG-----SW-----RRORQSVBEFPD 337  
DB 295 ACVRCVNPFLVAFIVKFRNDLFLKFKDGLGCLSQBLQWSSCRHRRSSMSVE----- 349  
QY 338 SEGPEPTSTFS 349  
DB 350 ---AETTTTFS 357

RESULT 9  
US-09-299-843A-19

; Sequence 19, Application US/09299843A  
; Patent No. 6107475  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Schweikart, Vicki L.  
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/088,337  
FILING DATE: 01-JUN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/153,848  
FILING DATE: 17-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: J111 E. Uhl  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/32059B  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX:

INFORMATION FOR SEQ. ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 358 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3; Length 358;  
Best Local Similarity 38.7%; Pred. No. 7e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALEONQSTDYEEENMGNTYDYSOYELICIKEDYREPAKVPFLPFLITVIVIGLAGNS 60  
DB 1 VCLCODEVTDDYIDGNT--TVDYTLFESLCSKDVNRKAWFLPTMYSIICFVGLGNG 57  
QY 61 MVVAIYAYYKORTKTVDYILNLAADVADLLFTLPMAVNAVHGVGLGIMCKITSALYT 120  
DB 58 LVVLTYYIKRLKMTDYLNLAVADILFLTLTPMAVSAKSWFGVHFCGLIPAIYK 117  
QY 121 LNFVSGMQLACISIDRYAVATKVP--QSGVGKPCWIIICVWMAAILSLIPOLVY 176  
DB 118 MSFSGMMLLLCISIDRYAVAIQAVSAHRHRAVLLISKSCVGIWILATVISIPELVS 177  
QY 177 TVNDNA-----RCIPFPRLYLGTSKALIQMEICIGFVVPPLINGVCFTIARTLMKP 231  
DB 178 DLORSSSEQAMRCSLITTEH---VEAFITIOVQMWIGFVPLPAMSFCVLVIIRTLQAR 234  
QY 232 NIKISRPLKVLTVVIFVITQLPYNIYKFCRAIDIIYSLITSCKMSKMDIAIOVTEST 291  
DB 235 NEBRKAIVITAVVVFIVFQLPYNGVLAQTVANFNITSSITCSELKOLNIAVDYTSI 294  
QY 292 ALFHSGLNLDILYVFMGASPKYVMVAKKYG-----SW-----RRORQSVBEFPD 337  
DB 295 ACVRCVNPFLVAFIVKFRNDLFLKFKDGLGCLSQBLQWSSCRHRRSSMSVE----- 349  
QY 338 SEGPEPTSTFS 349  
DB 350 ---AETTTTFS 357

RESULT 10  
US-09-088-337B-19  
; Sequence 19, Application US/09088337B  
; Patent No. 6348574  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; Gray, Patrick W.  
; Schwaikart, Vicki L.  
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,337B  
; FILING DATE: 01-Jun-1998  
; CLASSIFICATION: <Unknown>  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,848  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6348574and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 358 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-088-337B-19  
Query Match 36.2%; Score 659; DB 3; Length 358;  
Best Local Similarity 38.7%; Pred. No. 7e-49;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;  
QY 1 M A L E O N O S T D Y Y E E N K G T D Y S O Y E L I C K E D V R E P A K Y F L P V L I V T V I G L A G S 60  
DB 1 V C L C D E V T D D I G N T --- T V D Y T L F E S L C S K D V R N F K A M F L P T M Y S I I C F V G L L G N G 57  
QY 61 M V V A I Y A Y Y K K O R T K T D V Y I L N L A V A D L L L F T L P F M A V N A V H G V L G I M K I T S A L Y T 120  
DB 58 L V V L Y I Y F K R L K T M T D Y I L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I P A I Y K 117  
QY 121 L N F V S G M O F L A C I S I D R Y V A V T K P S --- Q S G V G P C W I I C F C V M A A I L S I P O L V Y 176  
DB 118 M S F F S G M L L L C I S I D R Y A I V Q A V S A H R H R A R V L I S L S C V G I W I L A T V I S I P E L L Y S 177  
QY 177 T Y N D N A --- R C I P F P R Y L G T S M K A L I O M E I C I G F V V P L I N G V C F I T A R T L M K M P 231  
DB 178 D I O R S S S E Q A M R C S I T T E H --- V E A P I T T I O V A M V I G F L V P L A M S F C Y L V I I R T L L Q A R 234  
QY 232 N I K I S S P L A V L T V V I F I V T O L P Y N I V F C R A I D I I Y S L I T S C N N S K M D A I O V T E S T I 291  
DB 235 N E R K A I V I T I A V V V F I V F O L P Y N G V L A Q I V A N F N I T S T C E L S K O L N I A Y D V T Y S L 294

QY 292 A L F H S C L N P I L Y E M G A S F K N Y W M K V A K Y G ----- S W ----- R R O R S V E E P P D 337  
DB 295 A C V R C C V N P F L Y A F I G V F R N D L F P L F R D L G L S O E O L R O W S S C H R I R S S M S V E ----- 349  
QY 338 S E G P T E P T S T S 349  
DB 350 --- A E T T T T S 357  
RESULT 11  
PCT-US93-11153-19  
; Sequence 19, Application PC/TUS9311153  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; Gray, Patrick W.  
; APPLICANT: Schwaikart, Vicki L.  
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Bicknell  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/11153  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 358 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US93-11153-19  
Query Match 36.2%; Score 659; DB 5; Length 358;  
Best Local Similarity 38.7%; Pred. No. 7e-49;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;  
QY 1 M A L E O N O S T D Y Y E E N K G T D Y S O Y E L I C K E D V R E P A K Y F L P V L I V T V I G L A G S 60  
DB 1 V C L C D E V T D D I G N T --- T V D Y T L F E S L C S K D V R N F K A M F L P T M Y S I I C F V G L L G N G 57  
QY 61 M V V A I Y A Y Y K K O R T K T D V Y I L N L A V A D L L L F T L P F M A V N A V H G V L G I M K I T S A L Y T 120  
DB 58 L V V L Y I Y F K R L K T M T D Y I L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I P A I Y K 117  
QY 121 L N F V S G M O F L A C I S I D R Y V A V T K P S --- Q S G V G P C W I I C F C V M A A I L S I P O L V Y 176  
DB 118 M S F F S G M L L L C I S I D R Y A I V Q A V S A H R H R A R V L I S L S C V G I W I L A T V I S I P E L L Y S 177  
QY 177 T Y N D N A --- R C I P F P R Y L G T S M K A L I O M E I C I G F V V P L I N G V C F I T A R T L M K M P 231  
DB 178 D I O R S S S E Q A M R C S I T T E H --- V E A P I T T I O V A M V I G F L V P L A M S F C Y L V I I R T L L Q A R 234

[illegible]

RESULT 12  
US-08-153-848-15  
; Sequence 15, Application US/08153848  
; Patent No. 5759804  
; Patent No. 5759804

```

1  APPLICANT: Godieka, Ronald
2  APPLICANT: Gray, Patrick W.
3  APPLICANT: Schweikart, Vicki L.
4  TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
5  NUMBER OF SEQUENCES: 64
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
8  ADDRESSEE: Bicknell,
9  STREET: 6300 Sears Tower, 233 South Wacker Drive
10 CITY: Chicago
11 STATE: Illinois
12 COUNTRY: USA
13 ZIP: 60606
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/153,848
22 FILING DATE:
23 CLASSIFICATION: 514
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/977,452
26 FILING DATE: 17-NOV-1992
27 ATTORNEY/AGENT INFORMATION:
28 NAME: No. 5759804and, Greta E.
29 REGISTRATION NUMBER: 35,302
30 REFERENCE/DOCKET NUMBER: 31794
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (312) 474-6300
33 TELEFAX: (312) 474-0448
34 TELEX: 25-3856
35 INFORMATION FOR SEQ ID NO: 15:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 378 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41
42 US-08-153-848-15

```

Query Match	Score	DB 1;	Length
36.2%	659;	DB 1;	378;
38.7%	659;	DB 1;	378;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

Db Qy 1 M A L E B Q N S T D Y Y E E N E M N G T Y V S Q Y E I C I K E D V R E A P K A V P L P E L T I F V I G I A G N S 60  
21 V C L C O E V T D Y I G D N T -- T V D Y T L F E S L C S K D V R N F A M P L P M Y S I I C F V G L I G N G 77

Db 21 VCLCQDEVTDYIGDNT---TVDYTLFESLCSKDVNRNFKAWFLPIMYSIICFVGGLGNG 77

61 MVAIYAYKKORTKDPYILNLAVADLLLEFLPFMAVNAVHGWLGKIMCKITSALYT 120

79 IYU TVYVEKBI KTMCTVYI I NI AIVDITI EI I TI DEWAVEA KSWIECUEKCI TEATYV 1327

QY 121 LNFVSGMQLACISIDRYVAVTKPS---QSGVGKPCWICFCVMAAILLSIPQLVFY 176

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Db      138 MSFSGMILLLLCISIDRYVAIVQAVSAHRHRARVLLSKLSCVGIWILATVLSIPILLYS 197
Qy      177 TVNDNA-----RCIPFPKYLGTSMKALLIMLEIGCVSPFLMGVCYFITAATLKMMP 231
Db      198 DLRSSSEQAMRSLLTEH---VEAFPTIQVQWIGFVPLBLSMFCVLIYITRLQAR 254
Qy      232 NIKISBPRLKVLTVIVIPVITOLPYNIYKFCRAIDIIYSLITSCMSKRMIDIAQVTEST 291
Db      255 NPERNNAIKIIVAVVVVFIPLQPLPYNGVLLQVTANFNITSTCELSQOLMIADVYSL 314
Qy      292 ALPHSCINPLILYVFMGSAFKYVMKVAKKYG-----SW-----RROQSEVEEPPD 337
Db      315 ACRRCCVNPFLVAFISVKFRNDLFLFLFDLGLGSLGSEQLRQMSOCHRIIRSSMSVBE----- 369
Qy      338 SEGPTPTSTFS 349
Db      370 ----AETTFPS 377

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Db 370 ----AETTTTFS 377

RESULT 13  
US-09-299-843A-15  
; Sequence 15, Application US/09299843A

? GENERAL INFORMATION :  
 ? APPLICANT: Godiska, Ronald  
 ? APPLICANT: Gray, Patrick W.  
 ? APPLICANT: Schweikart, Vicki L.  
 ? TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptor  
 ?  
 ? NUMBER OF SEQUENCES: 66  
 ?  
 ? CORRESPONDENCE ADDRESS :  
 ?

ADDRESS: Marshall, O'Toole, Murray &  
ADDRESS: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,843A  
FILING DATE:

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? CLASSIFICATION: 445
?
? PRIOR APPLICATION DATA:
?
? APPLICATION NUMBER: US 09/088,333
?
? FILING DATE: 01-JUN-1998
?
? PRIOR APPLICATION DATA:
?
? APPLICATION NUMBER: US 08/153,848
?
? FILING DATE: 17-NOV-1993
?
? PRIOR APPLICATION DATA:
?

```

APPLICATION NUMBER: US 07/977,452  
FILING DATE: 17-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: JILL E. Uhl  
REGISTRATION NUMBER: 43,213  
REFERENCE/DOCKET NUMBER: 27866/32059  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300

TELEX:

SEQUENCE CHARACTERISTICS:

LENGTH: 3/8 amino acids  
TYPE: amino acid

TOPOLOGY: linear

US-09-299-843A-15

Query Match 36.2%; Score 659; DB 3; Length 378;

Best Local Similarity 38.7%; Pred. No. 7,4e-49;  
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

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QY 1 MLEBONOSTDYEEENKMGTDYSGYELICKEDEYREPAKVFLLPVFLTIIVGIGLAGNS 60
DB 21 VCLCODEVTDYIDGNT---TVDYTLFESLCSKQDVNRKAMFLPIMYSIICFVGLGNG 77
QY 61 MVAIAYAYKKORTKTDVYILNLAIVADLLFLTPFWANAVHGWTLGIMCKITSALYT 120
DB 78 LVLLTYIYFKRLKTMIDTYILNLAIVADILFLTLFPWASAKSWFGVHPCFLIPAIRK 137
QY 121 LNFVSGMOFLACISIDRYAVATKVPB---QSGVGKPCWIIICFCVMAAILLISIPOLVY 176
DB 138 MSFFSGMLLLICSIDRYAIVQAVSAHHRARVLLISKLSCGVIIILATVLSIPELYS 197
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICGFVPPFLMGVCYFIARTLMKMP 231
DB 198 DIQRSSSEQAMRCSLITTEH---VEAFITIQVQWVGFLVPLPAMSFCYLVIIIRTLQAR 254
QY 223 NIKISRPLKVLTVIVFIVTQLPYNIKFCRAIDIIYSILTSCKMSKMDIAIQVTESEI 291
DB 255 NERNKAIVIIAVVVVFIVFQLPYNGVLAQTVANFNITSTCSELKQNLAIYDVITYSL 314
QY 292 ALFHSCLNPILYVFMGASFRTYMKVAKKYG-----SW-----RRQOSVEEPPD 337
DB 315 ACVRCVNPFLYAFIGVFRNDLFLKFDGLGCLSQEQLRWSSCRHRRSSMSVE----- 369
QY 338 SEGPTEPSTPS 349
DB 370 ----AETTTFS 377
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## RESULT 14

US-09-251-545-1  
; Sequence 1, Application US/09251545  
; Patent No. 6153441  
; GENERAL INFORMATION:  
; APPLICANT: Edward R. Appelbaum  
; APPLICANT: Henry M. Sarau  
; APPLICANT: John R. White  
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND  
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR  
; FILE REFERENCE: P50753  
; CURRENT APPLICATION NUMBER: US/09/251,545  
; FILING DATE: 1999-02-17  
; EARLIER APPLICATION NUMBER: 60/074,883  
; EARLIER FILING DATE: 1998-02-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 378  
; TYPE: PRT  
; ORGANISM: Human  
US-09-251-545-1

Query Match 36.2%; Score 659; DB 3; Length 378;  
Best Local Similarity 38.7%; Pred. No. 7,4e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

```
QY 1 MLEBONOSTDYEEENKMGTDYSGYELICKEDEYREPAKVFLLPVFLTIIVGIGLAGNS 60
DB 21 VCLCODEVTDYIDGNT---TVDYTLFESLCSKQDVNRKAMFLPIMYSIICFVGLGNG 77
QY 61 MVAIAYAYKKORTKTDVYILNLAIVADLLFLTPFWANAVHGWTLGIMCKITSALYT 120
DB 78 LVLLTYIYFKRLKTMIDTYILNLAIVADILFLTLFPWASAKSWFGVHPCFLIPAIRK 137
QY 121 LNFVSGMOFLACISIDRYAVATKVPB---QSGVGKPCWIIICFCVMAAILLISIPOLVY 176
DB 138 MSFFSGMLLLICSIDRYAIVQAVSAHHRARVLLISKLSCGVIIILATVLSIPELYS 197
QY 177 TVNDNA-----RCIPFPRYLGTSMKALIQMLEICGFVPPFLMGVCYFIARTLMKMP 231
```

```
DB 198 DIQRSSSEQAMRCSLITTEH---VEAFITIQVQWVGFLVPLPAMSFCYLVIIIRTLQAR 254
QY 223 NIKISRPLKVLTVIVFIVTQLPYNIKFCRAIDIIYSILTSCKMSKMDIAIQVTESEI 291
DB 255 NERNKAIVIIAVVVVFIVFQLPYNGVLAQTVANFNITSTCSELKQNLAIYDVITYSL 314
QY 292 ALFHSCLNPILYVFMGASFRTYMKVAKKYG-----SW-----RRQOSVEEPPD 337
DB 315 ACVRCVNPFLYAFIGVFRNDLFLKFDGLGCLSQEQLRWSSCRHRRSSMSVE----- 369
QY 338 SEGPTEPSTPS 349
DB 370 ----AETTTFS 377
```

## RESULT 15

US-09-088-337B-15  
; Sequence 15, Application US/09088337B  
; Patent No. 6348574  
; GENERAL INFORMATION:  
; APPLICANT: Godiska, Ronald  
; Gray, Patrick W.  
; Schenkert, Vicki L.  
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/088,337B  
; FILING DATE: 01-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/153,848  
; FILING DATE: 17-NOV-1993  
; APPLICATION NUMBER: US 07/977,452  
; FILING DATE: 17-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6348574and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 378 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-088-337B-15

Query Match 36.2%; Score 659; DB 3; Length 378;  
Best Local Similarity 38.7%; Pred. No. 7,4e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

```
QY 1 MLEBONOSTDYEEENKMGTDYSGYELICKEDEYREPAKVFLLPVFLTIIVGIGLAGNS 60
DB 21 VCLCODEVTDYIDGNT---TVDYTLFESLCSKQDVNRKAMFLPIMYSIICFVGLGNG 77
```

```
Qy 61 MVAIYAYYKORTKTDVYILNLAVADLLFLTPFMAVNAVHGVIGKIMCKITSALYT 120
Db 78 LVVLTFTYIFKRLKMTDFTLNLAVADILFLTLTPFMAVSAKSWFGVHFKLIFAIRK 137
Qy 121 LNFVSGMOPLACISIDRYVAVTKVPS---QSGVGKPCWIIICFCVMAAILLSIPOLVY 176
Db 138 MSFFSGMILLICISIDRYVAIVQAVSAHHRARVLLISKLSCVGIWILATVLSIPELYS 197
Qy 177 TVNDNA----RCIPFFPRYLGTSMKALOMLEICIGFVPPFLMGVCYFITARTLMKP 231
Db 198 DLQSSSEQAMRCSLITEH--VEAFITIQVAMVIGFLVPLLAMSFCYLVITIRTLQAR 254
Qy 232 NIKISRPLKVLTVVIVFIVTOLPVNIVKFCRAIDIIYSLITSNNMSKMDIAIQVTESI 291
Db 255 NFERNKAIKIVILAVVVVFIIVFQLPYNGVVLQAVANFNITSSCELSKQNLAYDYTSL 314
Qy 292 ALPHSCNLPILYVFMGASFKNYVMKVAKKYG-----SW-----RRQROSVEEFPPD 337
Db 315 ACVRCCVNPFLYAFIGVKFRNDLFKLFDGLGCLSQEQLRQWMSCRHIRRSSMSVE----- 369
Qy 338 SEGPTEPTSTFS 349
Db 370 ---AETTTTFS 377
```

Search completed: March 2, 2005, 04:23:33  
Job time : 25 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:13:51 ; Search time 19 Seconds  
(without alignments)  
1772.414 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819

Sequence: 1 MALBONOSTDYEEENENMG.....VEEFPDSBGPTEPTSTFSI 350

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	89.1	350	2 JN0621	G protein-coupled
2	659	36.2	378	2 B55735	Lymphocyte-specific
3	650	35.7	378	2 A55735	G protein-coupled
4	643	35.3	378	2 A45680	G protein-coupled
5	583	33.1	369	2 JCS068	G protein-coupled
6	537.5	29.5	360	2 A57160	chemokine (C-C) re
7	534.5	29.4	360	2 A53611	interleukin-8 rece
8	524	28.8	354	2 I58186	probable G protein
9	522.5	28.7	350	2 JCS04	orphan G protein-c
10	522.5	28.7	350	2 JCS04	chemokine (C-C) re
11	518.5	28.5	354	2 B55733	G protein-coupled
12	511	28.1	358	2 A53752	interleukin-8 rece
13	501.5	27.6	355	2 JQ1231	interleukin-8 rece
14	500.5	27.5	352	2 A45747	neuropeptide y/pep
15	499.5	27.5	353	2 S28787	neuropeptide y/pep
16	493.5	27.1	352	2 G00048	fusin (LESTRA) - c
17	492	27.0	360	2 JCS243	chemokine (C-C) re
18	489.5	26.9	350	2 A39445	interleukin-8 rece
19	486	26.7	355	2 JCS067	G protein-coupled
20	485	26.7	355	2 I49339	macrophage inflamm
21	484.5	26.6	352	2 A43113	chemokine (C-C) re
22	483.5	26.6	359	2 A48921	interleukin-8 rece
23	482	26.5	374	2 I38450	chemokine (C-C) re
24	479.5	26.4	359	2 I49341	MIP-1 alpha recept
25	476.5	26.2	367	2 JCS049	interferon-inducib
26	474	26.1	355	2 A45177	chemokine (C-C) re
27	471	25.9	356	2 S42096	interleukin-8 rece
28	470	25.8	383	2 S55594	G protein-coupled
29	461.5	25.4	355	2 G02436	chemokine (C-C) re

30	455.5	25.0	359	2 S44425	angiotensin II rec
31	452.5	24.9	359	2 JCI104	angiotensin II rec
32	452.5	24.9	359	2 JCI104	angiotensin II rec
33	450	24.7	359	2 S15403	angiotensin II rec
34	450	24.7	359	2 S32785	G protein-coupled
35	446.5	24.5	359	2 A48857	angiotensin II rec
36	445.5	24.5	356	2 I49340	MIP-1 alpha recept
37	442.5	24.3	372	2 S26667	G protein-coupled
38	442.5	24.3	374	2 S42628	G protein-coupled
39	441	24.2	362	2 JN0694	angiotensin II rec
40	439	24.1	359	2 A42656	angiotensin II rec
41	438.5	24.1	359	2 JH0621	angiotensin II rec
42	438.5	24.1	362	2 A39714	G protein-coupled
43	437.5	24.1	327	2 S56162	MDC15 protein - h
44	434	23.9	359	2 JQ516	angiotensin II rec
45	428.5	23.6	359	2 I39418	angiotensin II rec

#### ALIGNMENTS

##### RESULT 1

JN0621

G protein-coupled receptor type B - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004

C.Accession: JN0621

R.Matsuoka, T.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.

Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A.Title: Identification of novel members of G-protein coupled receptor superfamily expr

A.Reference number: JN0621; MUID:93326166; PMID:8392843

A.Accession: JN0621

A.Molecule type: mRNA

A.Residues: 1-350 <MAT>

A.Cross-references: UNIPROT:P35350; GB:S63848; NID:G399710; PIDN:AAB27547.1; PID:G399711

A.Experimental source: tongue taste papillae

C.Comment: This protein is involved in modulating taste sensitivity or regeneration of t

C.Superfamily: vertebrate rhodopsin

C.Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F/42-66/Domain: transmembrane #status predicted <TM1>

F/80-99/Domain: transmembrane #status predicted <TM2>

F/114-135/Domain: transmembrane #status predicted <TM3>

F/154-175/Domain: transmembrane #status predicted <TM4>

F/200-222/Domain: transmembrane #status predicted <TM5>

F/242-265/Domain: transmembrane #status predicted <TM6>

F/284-306/Domain: transmembrane #status predicted <TM7>

F/6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1% Score 1620; DB 2; Length 350;

Best Local Similarity 86.0% Pred. No. 1,1e-130; Mismatches 22; Indels 0; Gaps 0;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY	1	MALBONOSTDYEEENENMGTYDYSQYELICIKEDVREBAKFLPVFLTIVEVIGLAGNS	60
DB	1	MAVEYNOSTDYEEENENMDTHDYSQYEVICKEKVRKAKFLPAFFITATIGLAGNS	60
QY	61	MVAATYAYKKKRTTDTYIIMLAVALDLFTLPFAVANAHVGVLGKIMCKTSALYT	120
DB	61	TVAATYAYKKKRTTDTYIIMLAVALDLFTLPFAVANAHVGVLGKIMCKTSALYT	120
QY	121	INFVSGMOFLACISIDRYAAVTKVPDSQGVGRPCWITGCVMAAAILISIPOLVFYTVND	180
DB	121	VAFVSGMOFLACISIDRYAAVTKASQSGVGRPCWITGCVMAAAILISIPOLVFYTVNH	180
QY	181	NARCIPIPRVYGTSMKOLLQMLEICIGFVDFLMGVCFITATLMKMPKISRPX	240
DB	181	KARCVPIPRVYHGTSMKASIQLEICIGFIFLMACVFTATKLMMPKIKSQPX	240
QY	241	VLLTVVPIFYIYQLPYNIVKPRADIIYSLTSCMSKRMIAIQVESTLFFISCLNP	300
DB	241	VLETVVPIFYIYQLPYNIVKPCQALDIYSLTSDMSKRMVAIQIESTLFFISCLNP	300
QY	301	ILYVFMGASFKRYVMKAKKYGSMRQROSVBEPFDSBGPTEPTSTFSI	350

Db 301 VLYVFMGTSFKYIMKVKAKYGMWRQRQNVBEIPFESDADTEPTSTFSI 350

## RESULT 2

B55735

Lymphocyte-specific G protein-coupled receptor EB11 - human

N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004

C:Accession: B55735; S52443

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: B55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 &lt;SCH&gt;

A:Cross-references: UNIPROT:P32248; GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320

R:Bugstahler, R.; Kempkes, B.; Staube, K.; Lipp, M. submitted to the EMBL Data Library, February 1995

A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed

A:Reference number: S52443

A:Accession: S52443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 &lt;BUR&gt;

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 36.2%; Score 659; DB 2; Length 378;

Best Local Similarity 38.7%; Pred. No. 1.1e-48;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MALBQNSTDYEEENMGTYDYSQYELICKEDEVREPAKVFLLPVFLTVFVYIGLAGNS 60  
 DB 21 VCLCODEVTDDYIDGNT--TVDYTLFESLCSKDDVRFKAWFLPLMYSIIICFVGILGNG 77  
 QY 61 MVVAIYAYKKQRTKTDVYILMLAVADLLFTLPMAVNAVHGWLGKIMCKITSAIY 120  
 DB 78 LVVLYIYIKRLTMTDTYILMLAVADILFLTLTPMAVSAKSWVFGVHFKCLIPAIYK 137  
 QY 121 LNFVSGMOFLACISIDRYAVAVTKVP8-----QSGVGKPCWIIICFVWMAAILSLPOLV 176  
 DB 138 MSFSGMILLICISIDRYAVAIQAVSAHHRARVLLISLSCVGIWILATVLSIPELVS 197  
 QY 177 TVNDNA-----RCIPFPFYLTGSMKALIQMLEICIGFVVPFLMGVCYFITAATMKMP 231  
 DB 198 DLQSSSEQAMRCSLTTEH---VEAFITIQVQMWIGFVPLPAMSFVCLVIRTLQAR 254  
 QY 223 NIKISRLPLVLTIVVIFVITQLPYIVKFCRAIDIIYSLSCNMSKMDIAIQVTEGI 291  
 DB 255 NERNKATVITAVVVFIVFQIPNGVLAQTVANFNITSSICEISKQMLAIYDVYSL 314  
 QY 292 ALFHSCLNPLIYVFMGSAFKNYMKVAKYK-----SW-----RRQSGVEBFPDP 337  
 DB 315 ACVRCVCNPFVAFIVGKFRNDLFLKFDLGCLSGQLQWMSCRHRRSSMSVE----- 369  
 QY 338 SSGPTEPTSTFS 349  
 DB 370 ---AETTTTFS 377

## RESULT 3

A55735

G protein-coupled receptor EB11 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
 C:Accession: A55735  
 R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: A55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 &lt;SCH&gt;

A:Cross-references: UNIPROT:P47774; GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 35.7%; Score 650; DB 2; Length 378;

Best Local Similarity 38.3%; Pred. No. 6.6e-48;

Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8;

QY 5 QNSTDYEEENMGTYDYSQYELICKEDEVREPAKVFLLPVFLTVFVYIGLAGNSMVA 64  
 DB 25 QDEVTDDYIGENT--TVDYTLFESVCFKDDVRFKAWFLPLMYSVICFVGILGGLVIL 81  
 QY 65 IYAYKKQRTKTDVYILMLAVADLLFTLPMAVNAVHGWLGKIMCKITSAIYTLNV 124  
 DB 82 TYIYFRKLTMTDTYILMLAVADILFLTLTPMAVSEAKSWIFGVYLCGIRGITYKLSFF 141  
 QY 125 SGMQFLACISIDRYAVAVTKVP8QSG-----VGRKPCWIIICFVWMAAILSLPOLV 177  
 DB 142 SGMILLICISIDRYAVAIQAVSRHRARVLLISK---LSCVGIWILATVLSIPELVS 198  
 QY 178 VNDNA-----RCIPFPFYLTGSMKALIQMLEICIGFVVPFLMGVCYFITAATMKM 230  
 DB 199 LQKNSGEPLRC-----SLVSAQVBAITIIQAVQVFGFLVPLMAMSFVCLVIRTLQAR 253  
 QY 231 ENIKISRLPLVLTIVVIFVITQLPYIVKFCRAIDIIYSLSCNMSKMDIAIQVTEGI 290  
 DB 254 RNFERNKATVITAVVVFIVFQIPNGVLAQTVANFNITSSICEISKQMLAIYDVYSL 313  
 QY 291 IALFHSCLNPLIYVFMGSAFKNYMKVAKYGMWRQ-----QSVVEPFDSEGPTE 343  
 DB 314 LASVRCVCNPFVAFIVGKFRSDLFLKFDLGCLSGQERLRHMSCRHVNASVSM--AE 371  
 QY 344 PTSTFS 349  
 DB 372 TTTTFS 377

## RESULT 4

A45680

G protein-coupled peptide receptor EBI 1 - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A45680

R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E. J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled

A:Reference number: A45680; MUID:93188173; PMID:8383238

A:Accession: A45680

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-378 &lt;BIR&gt;

A:Cross-references: UNIPROT:P32248; GB:L08176; NID:g183484; PID:g183485

A:Experimental source: B-lymphocytes

A:Note: sequence extracted from NCBI backbone (NCBI:127094, NCBI:P.127095)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 35.3%; Score 643; DB 2; Length 378;

Best Local Similarity 39.0%; Pred. No. 2.6e-47;

Matches 145; Conservative 62; Mismatches 127; Indels 38; Gaps 8;

QY 1 MALBQNSTDYEEENMGTYDYSQYELICKEDEVREPAKVFLLPVFLTVFVYIGLAGNS 60

```
Db 21 VCLCODEVTDDYIGDNT---TVDYTLFESLCKKDVNFKAMFLPIMYSIICFVGLLNG 77
Qy 61 MVAIAYKKQRTKDVILNLAADLLFLPFAVNAVHGVNLGKIMCKITSAIYT 120
Db 78 LVVLTIVYERLKTMDYILNLAADILFLPFAVNAASWGVHFCILIPAIYK 137
Qy 121 LNFVSGMQLACISIDRYAVNTKVPQSOGVKPCWII--CFVWMA--AIIISIPOLVF 126
Db 138 MSFSGMILLICISIDRYAVIAVQAVSAHRARAVLISKSCVSAIATVLSIPELYS 197
Qy 177 TVNDNA-----RCIPFPRLGTSMKALIQMLEICIGFVFPFLIMGVCFITARTIMKP 231
Db 198 DQSSSEQAMRCSLITEH---VEAFITIQVAGMVGFLVPLAMSPCVIIRITLLQAR 254
Qy 232 NIKISPLKVLTVVFIYTOUPNIYKFCRAIDIIYSITSCNMSKMDIAIOTEST 291
Db 255 NERNKAIVIAVVFIVFOLPYNGVLAQTAVNFNITSCTELSKQINIVDYVYSL 314
Qy 292 ALPHSCLNPLIYFMGASPKNYVMKAKKYG-----SM-----RROROSVEPPFD 337
Db 315 ACRCVNPFLVAFIVKFRNDIPKLPKDLGCLSQEOLROMSSCRHRRSSMSVE----- 369
Qy 338 SEGPTEPTSTFS 349
Db 370 ---AETTTFS 377

RESULT 5
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JCS068
R:Abaillo, A.; Varona, R.; Galtier, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G
A:Reference number: JCS067, PMID:97040707, PMID:8886020
A:Accession: JCS068
A:Molecule type: DNA
A:Residues: 1-369 <TAB>
A:Cross-references: EMBL:279784; NID:91668737; PIDN:CA02144.1; PID:91668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 32.1%; Score 583; DB 2; Length 369;
Best Local Similarity 36.1%; Pred. No. 3.3e-42;
Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;
```

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Db 188 GSDVC---EPKQTVSEPIRWKILMLGTELLPEFPILPMFICFYFIKTVLQAQNSKR 244
Qy 236 SRPLKLLVNVVFIYTOUPNIYKFCRAIDIIYSITSCNMSKMDIAIOTESTALR 295
Db 245 HKAIRVIAVVFVFLCOIPHNMVLLVTAA--LGRNRSQSBKLYGTXTVEVLAFLH 303
Qy 296 SCINPLIYFMGASPKNYVMKAKKYGSWROROS 330
Db 304 CCLNPLVAFVIGQFRNRYFLKILKDLVCVRKYKS 338

RESULT 6
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A57160
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.;
J. Biol. Chem. 270, 19495-19500, 1995
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor C
A:Reference number: A57160; PMID:95370289; PMID:7642634
A:Accession: A57160
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <POM>
A:Cross-references: UNIPROT:P51679; GB:X85740; NID:91370103; PIDN:CAAS9743.1; PID:99714
A:Note: source clone KS-5
C:Genetics:
A:Gene: GDB:CMKBR4
A:Cross-references: GDB:677463
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:KeyWords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro
F:40-65/Domain: transmembrane #status predicted <TM1>
F:76-97/Domain: transmembrane #status predicted <TM2>
F:112-133/Domain: transmembrane #status predicted <TM3>
F:151-175/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:243-264/Domain: transmembrane #status predicted <TM6>
F:291-308/Domain: transmembrane #status predicted <TM7>
F:29-276.110-187/Diulfide bonds: #status predicted
F:72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predict
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:183.194/Binding site: carbodhydrate (Aan) (covalent) #status predicted
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 29.5%; Score 537.5; DB 2; Length 360;
Best Local Similarity 35.8%; Pred. No. 2.5e-38;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;
```



A:Experimental source: peripheral blood mononuclear cell  
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal  
C:Comment: This protein is a key regulator of many immune and homeostatic responses, and  
C:Genetics:  
A:Gene: v28  
A:Map position: 3pter-p21  
C:Superfamily: vertebrate rhodopsin  
F:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein  
F:35-57/Domain: transmembrane #status predicted <TM>  
F:66-88/Domain: transmembrane #status predicted <TM>  
F:104-125/Domain: transmembrane #status predicted <TM3>  
F:146-165/Domain: transmembrane #status predicted <TM4>  
F:197-217/Domain: transmembrane #status predicted <TM5>  
F:230-254/Domain: transmembrane #status predicted <TM6>  
F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match            28.7%   Score 522.5; DB 2; Length 355;  
Best Local Similarity   36.4%; Pred. No. 4.6e-37;  
Matches   112; Conservative   57; Mismatches   123; Indels   17; Gaps   5;

OY      22 VOISQVELICIKDVEFAKVPFLPVLITVIVIGLAGSNMVAIAYKKORTKDVIYL   81  
       ::::|::::|::::|::::|::::|::::|::::|::::|::::|::::|::::|  
DB      12 FEYDLAEACYSIDIVFGVTPLSFVSIFAIGVGMLVFALTNSKRKSVDIYLL   71  
       ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY      82 NLAVALDLLLFTLPFNAMNVHGMVLGKIMCKITSALTYLVNFSQMOPFIACSIRVVAV   141  
       ||:::||::||::||::||::||::||::||::||::||::||::||::||  
DB      72 NLALSLLLVATILPEFMTHYLINKEGLNNAMCKFTTAFPIFGSIFPTVISIDRYLAI   131  
       ||:::||::||::||::||::||::||::||::||::||::||::||::||

OY      142 TKVPS-----QSNGVKPCWIIICFYMAAILLSIPOLVETVNDNAKCIPIFRYYLT   194  
       :                :                :                :                :  
DB      132 VLAANSMNRRTVGHV----TSLGWAAAILVAAPQMFMTFKKEN--ECLGDYEVLGE   185  
       :                :                :                :                :

OY      135 SMKALIOMLEICGFVWPFLMGCVFITARTLMKPRIKSRPLKULLTVIVIFIVQL   254  
       |                :                :                :                :  
DB      186 IWPVANNTVNTPNFGLPLLIMSICYRRIIQTLSCKNHKAIAKLILLVIVFELFWT   245  
       :                :                :                :                :

OY      255 PYNIIVFCRAIDIIVSYLTSCTNMSKRMADIQVESIALFPSCNLPIVWFSGASPKNYV   314  
       ||:::||::||::||::||::||::||::||::||::||::||::||::||  
DB      246 PYNWMFLETLK-LYPDFSPCDMRKRLRALSVETVAFSHCCLNPLLIYAFAGERFRRL   304  
       ||:::||::||::||::||::||::||::||::||::||::||::||::||

OY      315 MKVAKKYG   322  
       :                :  
DB      305 YHL---YG   309

RESULT 10

JC4587  
chemokine (C-C) receptor 4 - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: Jc4587  
R:Hogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
A:Reference number: JC4587; PMID:96136324; PMID:8573157  
A:Accession: Jc4587  
A:Molecule type: mRNA  
A:Residues: 1-360 <HO>  
A:Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g116  
C:Genetics:  
A:Gene: cc ckr-4  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
F:2,183,194/Binding site: carbohydrate (asn) (covalent) #status predicted  
F:172,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred  
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match            28.7%   Score 522.5; DB 2; Length 360;  
Best Local Similarity   33.7%; Pred. No. 4.7e-37;  
Matches   110; Conservative   69; Mismatches   128; Indels   19; Gaps   6;

[illegible]

```

RESULT 11
B55733:
G protein-coupled receptor GPR2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
C:Accession: B55733
R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.
Genomic 23, 609-618, 1994
A:Title: Cloning of human gene encoding novel G protein-coupled receptors.
A:Reference number: A55733; MUID:9515483L; PMID:7851889
A:Accession: B55733
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <MAR>
A:Cross-references: GB:U13667
C:Genetics:
A:Gene: GDB:GPR2
A:Cross-references: GDB:371708; OMIM:600240
A:Map position: 17q21.1-17q21.3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match      28.5%; Score 518.5; DB 2; Length 354;
Best Local Similarity 33.9%; Pred. No. 1e-36;
Matches 121; Conservative 65; Mismatches 142; Indels 29; Gaps 7;

Oy      12  YYENENMGVYDSQVELLCIKREYRFAKVPFLVFLITYFVGLAGNSMVAIYAYKK 70
Db      5  HYSDE-EDAYSAPLELCYKADVQFSPAFQPSVLTVAALGLAGNGLVLTHTLAARR 63
Oy      71  KQRTKTVVLTINLAVDLLLTLPFWAANAAGWVVGKIMCKITSALTYNFVSGQFL 130
Db      64  AARSPFIAHLQLALADULLLTLPFAAALQGSLSGASTCRITSLVYASFPAGLFL 123
Oy      131  ACISIDRYVAATKY----PSQSGVKRCPWITICFVMAAILLSIPOLVFTYVND--NAR 183
Db      124  ACISADRYVAIARLPAQPRPSTFGR-AHLVSVYVMLSTLLALPALLFQDQREGQRR 182
Oy      184  CIPFPFVLTSMKALIQMLEICGFVVPFLINGVCFFIARTLTKMPNIKIRPLKVL 243
Db      183  CRLLFPGLQLQTVAGASAVNQVALGFALPLGVMAVACALIGRTLAAFGERRRALRVV 242
Oy      244  TVVIVFIVTQLPYVIVFCRAIDIIYSLITSCMMSKMDIAIQVTESIALFHSCLNPILY 303
Db      243  ALVAAPFVVLQPLPSIALLLDTADLLAARENSCPASRKRQDVALLVTSGLALARGCLNPVLY 302
Oy      304  VFWGASFKNTVMKYAK-----KYGSWRQROSVVEEFPDSDGPTPEPTSTFSI 350
Db      304  VFWGASFKNTVMKYAK-----KYGSWRQROSVVEEFPDSDGPTPEPTSTFSI 350

```

Db 303 AFLGPFRODLRLRLRGSSPSGPOPRRCGPRRPRRLS-----SCSAPETHTSL 350

# RESULT 12

AS3752

Interleukin-8 receptor (clone 5B1a) - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #ext\_change 09-Jul-2004

C/Accession: AS3752

R.Prado, G.N.; Thomas, K.M.; Suzuki, H.; Larosa, G.J.; Wilkinson, N.; Folco, E.; Navarro

J. Biol. Chem. 269, 12391-12394, 1994

A/Title: Molecular characterization of a novel rabbit interleukin-8 receptor isoform.

A/Reference number: AS3752; MUID:94230294; PMID:8175642

A/Accession: AS3752

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-358 <PDB>

A/Cross-references: UNIPROT:P35344; GB:U24445; NID:g437661; PIDN:AAA31378.1; PID:g437662

C/Suprafamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.1%; Score 511; DB 2; Length 358;  
Best Local Similarity 32.3%; Pred. No. 4,5e-36;  
Matches 116; Conservative 72; Mismatches 139; Indels 32; Gaps 8;

10 DYVEENENMGNTYDSQVELI-----CIKEDVEFAKVPVPLTIVFVIGLA 57

8 NYSYE--DFPG--DEFNYSYSTDLPTLLDSAPCESLETNSYVLLIYI-LVFLSL 62

58 GNSMVVAIYAYKKQRTQDVILNLAVADLLFLTPFVAANAHHGVGKIMCKITSA 117

63 GNSLWMLVILYRSSTCSVDVLLNLAIADLLFATLLPTMAASKVHGFPGPLCKVSL 122

118 LVTINPVSOGMOFLACISIDRYAV-----TKVPSOSGKPCWIIICFCVMAAILSTIQ 172

123 VAEVNFYSGLILACISVRYALIVHATRTMOKRLVK---PILSMGVSLIISLP 178

173 LVFVYVNDNARCIPIPRYIGTS---MKALIQMLEICGFVVPFLMGVCYFTARTLTK 229

179 LIFRNAIFPNSSPVCEDMGSTAKRWAVRLPOTPFILPLVLMFCYVETLTLTQ 238

230 MNKISRLPKVLLTVIVIVITQDPYNTVYKFCRAIDIIYSLTSCNMSKMDIAIQVTE 289

239 AHMGQKRRMARVFAVVLFLFCWLPYNNVLLDTLMRTHVIOETCERRNDIDRALDATE 298

290 STALFSCSNPIITLYVMGASFKYVWKVKKYGSWRQ---RQSVSEFPDSDGPRTEPT 345

299 ILGFLHSCNPIITVAFYTGKFRYGLKILIAHGLISKEPLAKSRPSFVASSSGNTSTT 357

Db

RESULT 13

JO1231

Interleukin-8 receptor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #ext\_change 09-Jul-2004

C/Accession: JO1231; A46483

R.Beckmann, M.P.; Mungler, W.E.; Kozlosky, C.; Vandenbos, T.; Price, V.; Lyman, S.; Gerard

Biochem. Biophys. Res. Commun. 179, 784-789, 1991

A/Title: Molecular characterization of the interleukin-8 receptor.

A/Reference number: JO1231; MUID:91378994; PMID:1898400

A/Accession: JO1231

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-355 <BEC>

A/Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439

R.Isee, J.; Khang, W.J.; Rice, G.C.; Wood, W.I.

J. Immunol. 148, 1261-1264, 1992

A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.

A/Reference number: A46483; MUID:92148149; PMID:1737938

A/Accession: A46483

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-355 <DEB>

A/Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441

A/Experimental source: neutrophils  
A/Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)  
C/Suprafamily: vertebrate rhodopsin  
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 501.5; DB 2; Length 355;  
Best Local Similarity 33.1%; Pred. No. 2.9e-35;  
Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

12 YVEENENMGNT-----YDSQVELI-----CIKEDVEFAKVPVPLTIVFVIGLAGSMVVAI 65

14 WEDVEFANATGMPPEKYS--PCLIVTQTLKVVV--VYALVFLSLGLNLMKV 68

66 YAYVKQRTQDVILNLAVADLLFLTPFVAANAHHGVGKIMCKITSAVLTNLFVS 125

69 ILYSRNSNSVDVILNLAMADLLPALMTPVAVASKEKMGIRGTLCKVSLVKEVNFYS 128

126 GNOFLACISIDRYAV-----TKVPSOSGKPCWIIICFCVMAAILSTIQVLYTYNDNA 182

129 GILLIACISVDRYALIVHATRTLTQK--RHLVKFICLGIMALSTILSLPFLRFQVFSFN 186

183 RCIPFPRYIG--TSMKALIQMLEICGFVVPFLMGVCYFTARTLTKMKNISRL 239

187 NSSPVCYEDLGNTAKRWVRLIHPHTGFILPLVLMFCYFTRTLFQAMGQKRRM 246

240 KVLTVIVIVITQDPYNTVYKFCRAIDIIYSLTSCNMSKMDIAIQVTEIALPHSCIN 299

247 RVIFAVVILFLCWLPPYMLVLLADTLMTHTVIOETCERRNDIDRALDATEILGLHSCIN 306

300 PLIYVFMGASFKYVWKVKKYGS 322

307 PLIYAFIGQNFNGFLKMLAARG 329

Db

RESULT 14

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N/Alternate names: fusin; HM99; leukocyte-derived seven-transmembrane receptor LESTR; re

C/Species: Homo sapiens (man)

C/Date: 03-May-1994 #sequence\_revision 03-May-1994 #ext\_change 09-Jul-2004

C/Accession: A45747; A53103; I53006; I59444; I69203; S13761

R.Federber, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis

Genomics 16, 707-712, 1993

A/Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu

A/Reference number: A45747; MUID:93315164; PMID:8325644

A/Accession: A45747

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-352 <PDB>

A/Cross-references: UNIPROT:P61073; GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g292517

R.Loetscher, M.; Geisler, T.; O'Reilly, T.; Zwaehlen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A/Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly c

A/Reference number: A53103; MUID:94103215; PMID:8276799

A/Accession: A53103

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-352 <DEB>

A/Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100

R.Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.

DNA Cell Biol. 12, 465-471, 1993

A/Title: Molecular cloning, characterization, and localization of the human homolog to t

A/Reference number: I53006; MUID:93319629; PMID:8329116

A/Accession: I53006

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-352 <HER>

A/Cross-references: GB:U66797; NID:g414929; PIDN:AAA03209.1; PID:g414928

R.Islaz, B.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; Lar

Regul. Pept. 47, 247-258, 1993

A/Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo

A/Reference number: I59444; MUID:94052893; PMID:8234909

A/Accession: I59444

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:14:37 ; Search time 66 seconds  
(without alignments)  
2715.571 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819  
Sequence: 1 MALEGNQSDYYEENMNG.....VEFPDSDSGPTPTSTFSI 350

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_aprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	1 CKRB_HUMAN	Q9nb9 homo sapien
2	1620	89.1	350	1 CKRB_BOVIN	P35350 bos taurus
3	1586	87.7	350	2 Q92A13	Q92A13 mus musculu
4	1594	87.6	350	2 Q8C0M1	Q8C0M1 mus musculu
5	1593	87.6	350	2 Q8QZM9	Q8QZM9 mus musculu
6	1070	58.8	356	2 Q63ZL5	Q63ZL5 xenopus lae
7	912	50.1	221	2 Q9SEK1	Q9SEK1 rattus norv
8	663	36.4	369	2 Q6Y747	Q6Y747 sus scrofa
9	659	36.2	378	1 CKR7_HUMAN	P32248 homo sapien
10	657	36.1	357	2 Q6Y746	Q6Y746 sus scrofa
11	657	36.1	378	2 Q8H2R6	Q8H2R6 macaca mula
12	650	35.7	378	1 CKR7_MOUSE	P47774 mus musculu
13	649	35.7	358	2 Q6G958	Q6G958 xenopus lae
14	648	35.6	378	2 Q8C8A2	Q8C8A2 mus musculu
15	646	35.5	378	2 Q6U2D6	Q6U2D6 rattus norv
16	645.5	35.5	380	2 Q8G1S1	Q8G1S1 sus scrofa
17	643	35.3	369	2 Q9UQ06	Q9UQ06 homo sapien
18	643	35.3	369	2 Q8CH33	Q8CH33 rattus norv
19	639	35.1	369	1 CKR9_MOUSE	Q9m733 mus musculu
20	637	35.0	357	1 CKR9_HUMAN	P51866 homo sapien
21	629.5	34.6	382	2 Q702H3	Q702H3 gallus gall
22	612.5	33.7	325	2 Q677Y8	Q677Y8 lymphocysti
23	611	33.6	367	2 Q9R1V0	Q9R1V0 mus musculu
24	608.5	33.5	369	2 Q76LH9	Q76LH9 paralichthy
25	605	33.3	367	1 CKR6_MOUSE	Q54689 mus musculu
26	598	32.9	341	2 Q6Y744	Q6Y744 sus scrofa
27	586.5	32.2	368	2 Q42444	Q42444 oncorhynch
28	583	32.1	374	1 CKR6_HUMAN	P51684 homo sapien
29	583	32.1	374	2 Q8H2R7	Q8H2R7 macaca mula
30	581	31.9	342	1 CKR6_CERAE	Q18983 cercopithe
31	578	31.8	343	2 Q9N0Z0	Q9N0Z0 cercocebus

32	571	31.4	343	1 CKR6_MACMU	Q9xc45 macaca mula
33	569	31.3	342	1 CKR6_MACNE	Q19024 macaca neme
34	566.5	31.1	351	2 Q9S016	Q9S016 mus musculu
35	566	31.1	343	1 CKR6_MACPA	Q9b066 macaca faec
36	561.5	30.9	351	2 Q9SRH5	Q9SRH5 mus musculu
37	560	30.8	333	2 Q678F3	Q678F3 lymphocysti
38	560	30.8	342	1 CKR6_HUMAN	Q00574 homo sapien
39	560	30.8	342	2 Q9HC45	Q9HC45 homo sapien
40	559	30.7	342	1 CKR6_PANTR	Q9rv16 pan troglod
41	544	29.9	358	2 Q9PUA0	Q9PUA0 acipenser t
42	537.5	29.5	360	1 CKR4_HUMAN	P51679 homo sapien
43	535.5	29.4	355	2 Q8H2N7	Q8H2N7 gorilla gor
44	534.5	29.4	355	2 Q8H2N6	Q8H2N6 pongo pygma
45	534.5	29.4	355	2 Q8H2N8	Q8H2N8 pan troglod

## ALIGNMENTS

RESULT 1  
ID CKRB\_HUMAN STANDARD, PRT, 350 AA.  
AC Q9NPB9;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11)  
DE (Chemokine receptor-like 1) (CCRL1) (CCX CKR).  
GN Name=CCRL1; Synonyms=CCBP2, CCR11, VSHK1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20200450; PubMed=10734104; DOI=10.1074/jbc.275.13.9550;  
RA Schweickart V.L.; Epp A.; Raport C.J.; Gray P.W.;  
RT "CCR11 is a functional receptor for the monocyte chemoattractant  
protein family of chemokines."  
RL J. Biol. Chem. 275:9550-9556 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20171478; PubMed=10706668;  
RA Goelling J.; Dairaghi D.J.; Wang Y.; Hanley M.; Talbot D.; Miao Z.;  
RA Schall T.J.;  
RT "Identification of a novel chemokine receptor that binds dendritic  
cell- and T cell-active chemokines including ELC, SLC, and TECK."  
RL J. Immunol. 164:2851-2856 (2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=2031748; PubMed=10767544; DOI=10.1016/S0378-1119(00)00076-7;  
RA Khoja H.; Wang G.; Ng C.-T.L.; Tucker J.; Brown T.; Shyamala V.;  
RT "Cloning of CCRL1, an orphan seven transmembrane receptor related to  
chemokine receptors, expressed abundantly in the heart."  
RL Gene 246:229-238 (2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Kopatz S.A.; Aronstam R.S.; Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
regulated by the G-protein coupled receptor (www.cdn.org).";  
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Receptor for SCY2/MCP1, SCY2/MCP2, SCY13/MCP4.  
CC SCY19/MIP3/ELC, SCY21/SIC and SCY25/TECK.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Predominantly expressed in heart. Lower  
expression in lung, pancreas, spleen, small intestine and fetal  
tissues.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL, AF193507; AAF61299.1; -;  
 DR EMBL, AF233281; AAF44751.1; -;  
 DR EMBL, AF110640; AAF59827.1; -;  
 DR EMBL, AY221094; AAO65972.1; -;  
 DR Genbank; HGNC.1611; CCRL1.  
 DR GO; GO:0005887; C.integral to plasma membrane; TAS.  
 DR GO; GO:0004950; P.chemokine receptor activity; TAS.  
 DR GO; GO:0006935; P.chemotaxis; TAS.  
 DR GO; GO:0007186; P.G-protein coupled receptor protein signalin. . .; TAS.  
 DR GO; GO:0006955; P.immune response; TAS.  
 DR InterPro; IPR005383; CC.11 receptor.  
 DR InterPro; IPR000355; Chkline receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1.1.  
 DR PRINTS; PRO1558; CHEMOKINER11.  
 DR PRINTS; PRO0237; GPCR\_RHODOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECP\_F1\_2; 1.  
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1  
 FT TRANSMEM 43  
 FT TRANSMEM 64  
 FT TRANSMEM 88  
 FT TRANSMEM 109  
 FT TRANSMEM 114  
 FT TRANSMEM 135  
 FT TRANSMEM 155  
 FT TRANSMEM 176  
 FT TRANSMEM 202  
 FT TRANSMEM 223  
 FT TRANSMEM 241  
 FT TRANSMEM 262  
 FT TRANSMEM 289  
 FT TRANSMEM 310  
 FT TRANSMEM 311  
 FT CARBOHYD 6  
 FT CARBOHYD 19  
 FT DISULFID 112  
 FT SEQUENCE 350 AA; 39913 MW; 8E26049D25757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-103;  
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYEEENENNGTDDYSEYELICIKEDVREPAKVPFLPVFLTIVFVIGLAGNS 60  
 DB 1 MALEONQSTDYEEENENNGTDDYSEYELICIKEDVREPAKVPFLPVFLTIVFVIGLAGNS 60  
 QY 61 MVAIAAYVKKORTKTDVYILNLAVALDILLFTLPWANAANAGWIGKIMCKTITALT 120  
 DB 61 MVAIAAYVKKORTKTDVYILNLAVALDILLFTLPWANAANAGWIGKIMCKTITALT 120  
 QY 121 LNFVSGMOFLACISIDRYAVAVTVPQSQGVGKPCWICFCVMAAAILLSIPOLVFTYND 180  
 DB 121 LNFVSGMOFLACISIDRYAVAVTVPQSQGVGKPCWICFCVMAAAILLSIPOLVFTYND 180  
 QY 121 LNFVSGMOFLACISIDRYAVAVTVPQSQGVGKPCWICFCVMAAAILLSIPOLVFTYND 180  
 DB 121 LNFVSGMOFLACISIDRYAVAVTVPQSQGVGKPCWICFCVMAAAILLSIPOLVFTYND 180  
 QY 181 NARCIPIPRYLGTSKMKALIQMLEICIGFVVPPLINGVCYFTARTLMKPNIKISRPLK 240  
 DB 181 NARCIPIPRYLGTSKMKALIQMLEICIGFVVPPLINGVCYFTARTLMKPNIKISRPLK 240  
 QY 241 VLLTVIVIVIVQLPNIYKFCRAIDIIYSLTSCMSKRMDAIOTVTSIALFHSCLNP 300  
 DB 241 VLLTVIVIVIVQLPNIYKFCRAIDIIYSLTSCMSKRMDAIOTVTSIALFHSCLNP 300  
 QY 301 ILYVFGASFKYVVMVAKKYGSROROSVEEFPDSEGPTEPTSTFSI 350  
 DB 301 ILYVFGASFKYVVMVAKKYGSROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 2

CKRB BOVIN  
 ID CKRB BOVIN STANDARD; PRT; 350 AA.  
 AC P35350;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE C-C chemokine receptor type 11 (C-C-CKR-11) (CC-CKR-11) (CCR-11)  
 DE (Possible gustatory receptor type B) (PpRI protein).  
 GN Name=CCRL1; Synonyms=CCR11;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCB1\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE= Tongue;  
 RX MEDLINE=9332616; PubMed=8392843;  
 RA Matsuoka I., Mori T., Aoki U., Sato T., Kurihara K.;  
 RT "Identification of novel members of G-protein coupled receptor  
 RT superfamily expressed in bovine taste tissue."  
 RL Biochem. Biophys. Res. Commun. 194:504-511(1993).  
 CC -1- FUNCTION: Receptor for SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,  
 CC SCYA19/MIP3B/ELC, SCYA21/SUC and SCYA25/TECK (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in circumvallate and fungiform  
 CC papillae, olfactory epithelium and lung. Lower expression in  
 CC liver, kidney and tongue epithelium bearing no taste papillae.  
 CC Very low expression in the cerebral cortex of the brain.  
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial/  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

Query Match

89.1%; Score 1620; DB 1; Length 350;

	Best Local Similarity	86.0%	Pred. No. 3,3e-91;	
Matches	301;	Conservative	27;	Mismatches 22; Indels 0; Gaps 0
Qy	1	MALEONOSTDYEEENENNGTYDSQYELICIKEDVREFAKYFLPEVLTIVFVIGLAGNS	60	
Db	1	MAVEYQNSTDYEEENENMDTHDYSQYEVICIKEEYRKFAKFLPAFFIAFTIIGLAGNS	60	
Qy	61	MVVAIYAYVKKORTSDYVYIINLAAVADILLTLPMPWANAHVGWLGKINCKITSALYT	120	
Db	61	TVVAIYAYVKKRRTKDVIYIINLAAVADLFLLTLPMPWANAHVGLGKICKVTSALYT	120	
Qy	121	LNPFVSGMOFLACISIDRYVAVTKVPSQSGVGKPCWIIICFCVMAAAILLSIPOLVFYTVND	180	
Db	121	VNPFVSGMOFLACISIDRWVAVTKAPSQSGVGKPCWICFCVVAAILLSIPOLVFYTVNH	180	
Qy	181	NARCIPIEPFRVYIGTSMKALIQMLEITICGFVVPPLIMGVCYFTTARTLMMPNIKISRLPK	240	
Db	181	KARCPVPIPPHYIGTSMKASIQILEITICGPIPLIMAVCYFTTAKTLIMPMNPKSQPLK	240	
Qy	241	VLLTVYVIFVYQLPYNIYKFCRAIDIIYSLTSCNMSGRMIOAIQVETESILPFSCLNP	300	
Db	241	VLFYTVYVIFVYQLPYNIYKFCQALDIITSLTDCMSGRMDVAYIOITISIALPFSCLNP	300	
Qy	301	ILYVFMGASFKNYVYKVKAKKYSWMRQRQSVSEPFPSBGPTEPTSTFSI	350	
Db	301	VLYVFMGTSFKNYIMKVAKKYSWMRQRQNVBEIPRESDATEPTSTFSI	350	
RESULT 3				
ID	Q924I3	PRELIMINARY;	PRT;	350 AA.
AC	Q924I3;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Chemokine receptor CCR11 (Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630091E18 product:CHEMOKINE RECEPTOR CCR11 homolog).			
DE	GN Name=Ccr11;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RC	MEDLINE=20519697; PubMed=11063828; DOI=10.1016/S0165-5728(00)00371-4;			
RA	"Dorf M.E., Betman M.A., Tanabe S., Heesen M., Luo Y.;			
RT	"Astrocytes express functional chemokine receptors.";			
RL	J. Neuroimmunol. 111:109-121(2000).			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RA	Luo Y., Betman M.A., Fischer F.R., Abramson-Jeeman S.R., Kuziel W.A.,			
RL	Geard C., Dorf M.E.;			
RN	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6679(99)03004-9;			
RA	Carnini P., Hayashiraki Y.;			
RT	"High-efficiency full-length cDNA cloning.";			
RL	Meth. Enzymol. 303:19-44(1999).			
RN	[4]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;			
RA	RIKEN FANTOM Consortium;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 403:685-690(2001).			
RN	[5]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Thymus;			

The PANTOM Consortium.

RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20499374; PubMed=11042153; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
Genome Res. 10:1617-1630(2000).

RN [7]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [8]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [9]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [10]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [11]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [12]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [13]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [14]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [15]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [16]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
Genome Res. 10:1157-1171(2000).

RN [17]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa W., Ohara E., Matsubiki M.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
Okazaki Y., Muramatsu M.,

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OY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWITICFCVMAAAILLSIPOLVFYTVND 180
DB 121 VNFVSGMOFLACISIDRYVAITKAPBSGAGRPCCWITICCVMAAAILLSIPOLVFYTVNQ 180
OY 181 NARCTPIFPFHLGTSTKASIOMLIEICIGFVFPFLIMGVCYFARTATMKPINKISRPDK 240
DB 181 NARCTPIFPFHLGTSTKASIOMLIEICIGFVFPFLIMGVCYFARTATMKPINKISRPDK 240
OY 241 VLLTVIVFIVTQLPYNIKFCRAIDIIYSLTSCMSRMDIAIOVTSIALFHSCLNP 300
DB 241 VLLAVVVFIVTQLPYNIKFCRAIDIIYSLTSCMSRMDIAIOVTSIALFHSCLNP 300
OY 301 ILYVFGASFKYIMVAKKYGSGWRQROSVBEPDSEGPTEPTSTFSI 350
DB 301 ILYVFGASFKYIMVAKKYGSGWRQROSVBEPDSEGPTEPTSTFSI 350

RESULT 4
O8COM1 PRELIMINARY; PRT; 350 AA.
ID AC O8COM1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
DE library, clone:5430400N1 product:CHEMOKINE RECEPTOR CCR11
DE homolog.
CN Name=Ccr11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA The PANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itch M.,
RA Kono H., Okazaki Y., Muramatsu N., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11078661; DOI=10.1101/gr.152600;
RA Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itch M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara-E., Wataniki M.,

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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraka T., Hirozawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kankawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saico R., Saich H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AK030643; BNC27061.1; -.
DR MGD: 2181676; Ccr11.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein-coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR005383; CC_11_receptor.
DR InterPro: IPR000355; Chemlike_receptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1.1; 1.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01558; CHEMOKINER1.
DR PRINTS: PR00237; GPCRRODOSEN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR KMW: G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 350 AA; 39562 MW; DAACD9D798EAS13 CRC64;

Query Match 87.6%; Score 1594; DB 2; Length 350;
Best Local Similarity 85.4%; Pred. No. 1.2e-89;
Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

OY 1 MLEQNSTDYEEENMGTYDYSQYELICKEDEVREKAYFLPVFLTIVFGLAGNS 60
DB 1 MLELNQSAHYEEENMGTYDYSQYELICKEDEVREKAYFLPVFLTIVFGLAGNS 60
OY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPWAVNAVHGVLAGKIMCKTISALT 120
DB 61 VVVAIYAYKKORTKTDVYILNLAVADLLFLTPWAVNAVHGVLAGKIMCKTISALT 120
OY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGKPCWITICFCVMAAAILLSIPOLVFYTVND 180
DB 121 VNFVSGMOFLACISIDRYVAITKAPBSGAGRPCCWITICCVMAAAILLSIPOLVFYTVNQ 180
OY 181 NARCTPIFPFHLGTSTKASIOMLIEICIGFVFPFLIMGVCYFARTATMKPINKISRPDK 240
DB 181 NARCTPIFPFHLGTSTKASIOMLIEICIGFVFPFLIMGVCYFARTATMKPINKISRPDK 240
OY 241 VLLTVIVFIVTQLPYNIKFCRAIDIIYSLTSCMSRMDIAIOVTSIALFHSCLNP 300
DB 241 VLLAVVVFIVTQLPYNIKFCRAIDIIYSLTSCMSRMDIAIOVTSIALFHSCLNP 300
OY 301 ILYVFGASFKYIMVAKKYGSGWRQROSVBEPDSEGPTEPTSTFSI 350
DB 301 ILYVFGASFKYIMVAKKYGSGWRQROSVBEPDSEGPTEPTSTFSI 350

RESULT 5
O8Q2W9 PRELIMINARY; PRT; 350 AA.
ID O8Q2W9

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AC 08QZM9;  
 DT 01-JUN-2002 (Tremblrel. 21, Created)  
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Chemokine receptor CCR1.  
 DE Chemokine receptor CCR1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10930;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Svj.  
 RA Thomson J.R., Nibbs R.J.  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AY072796; AAL68400.1; -  
 DR EMBL; AY072938; AAL68962.1; -  
 DR MGD; MG1:2181676; Ccr1l.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; IEA.  
 DR InterPro: IPR005383; CC\_11\_receptor.  
 DR InterPro: IPR000355; Chk1n\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01558; CHEMOKINER1.  
 DR PRINTS; PR00237; GPCR\_RHODOPN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_P1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_P1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 350 AA; 39544 MW; D017CC29749CECD5 CRC64;

Query Match 87.6%; Score 1593; DB 2; Length 350;  
 Best Local Similarity 85.1%; Pred. No. 1,4e-89;

Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNS 60  
 DB 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNS 60  
 QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMKITSALYT 120  
 DB 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMKITSALYT 120  
 QY 121 LMPVSGMOPLACISIDRYAVAVTKVPSQSGVKPCWIIICPCVMMAAIILSLPOLVFTTND 180  
 DB 121 LMPVSGMOPLACISIDRYAVAVTKVPSQSGVKPCWIIICPCVMMAAIILSLPOLVFTTND 180  
 QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLINGVCYFIFARTLMKPNIKISRPK 240  
 DB 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLINGVCYFIFARTLMKPNIKISRPK 240  
 QY 241 VLLTIVIVETQLPYNIVKPCRAIDIIYSLITSCMSKRMIDIAIQTESIALFHSCLNP 300  
 DB 241 VLLTIVIVETQLPYNIVKPCRAIDIIYSLITSCMSKRMIDIAIQTESIALFHSCLNP 300  
 QY 301 ILYVPMGASFKYVMVAKKYGWROROSVEFPDSDGPRPSTFPI 350  
 DB 301 ILYVPMGASFKYVMVAKKYGWROROSVEFPDSDGPRPSTFPI 350

RESULT 6

063ZL5 PRELIMINARY; PRT; 356 AA.

AC 063ZL5; 25-OCT-2004 (Tremblrel. 28, Created)  
 DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)  
 DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE Hypothetical protein.  
 OS Xenopus laevis (African Clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN 11)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dev.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative";  
 RL Dev. Dyn. 225:384-391(2002).

RN 12)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN 13)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Whole;  
 RX Klein S., Gerhard D.S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC082897; AAH82897.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 356 AA; 40514 MW; 2B4FAEA6561487A CRC64;

Query Match 58.8%; Score 1070; DB 2; Length 356;  
 Best Local Similarity 60.8%; Pred. No. 1e-57;

Matches 211; Conservative 49; Mismatches 81; Indels 6; Gaps 3;

QY 8 STDYEEENMGTYDSQYELICIKEDVREFAKFLPVFLTIVFVIGLAGNSMVAIYA 67  
 DB 12 TTEENDEYDGT--TPYGNVYBELCEKEVRQFAQIFLPFAVNAVFIAGVAGNSLVVAIYS 69  
 QY 68 YKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVGLKIMKITSALYTINLVSGM 127  
 DB 70 YKKMKSRTDVYILNLAVADLLFLTPFWAWDAAVGOFGIFMCKITSAIYINFSGG 129  
 QY 128 OFLACISIDRYAVAVTKVPSQSGVKPCWIIICPCVMMAAIILSLPOLVFTV--NNARC 184  
 DB 130 OFLACISIDRYAVAVTKVPSQSGVKPCWIIICPCVMMAAIILSLPOLVFTV--NNARC 189  
 QY 185 IPFPRYLGTSMKALIQMLEICIGFVVPFLINGVCYFIFARTLMKPNIKISRPKVLTL 244  
 DB 190 LPVYPRDKYKQTTLVLIQILEIVFCFLPLFVWVFCVSAVAKIVLTKPNIKRSRLKVLTA 249  
 QY 245 VVIVFIVTQLPYNIVKPCRAIDIIYSLITSCMSKRMIDIAIQTESIALFHSCLNPILV 304  
 DB 250 VVGVPFLVTLQPLYNIVKPCRAIDIIYSLITSCMSKRMIDIAIQTESIALFHSCLNPILV 309  
 QY 305 FNGASFKYVMVAKKYGWROROSVEFPDSDGPRPSTFPI 350

Db 310 FMGTFKCYISKIARCCSLRQRJHSTEEFSGHSEBNHVEFTSSFSI 356

## RESULT 7

Q9ESK1 PRELIMINARY; PRT; 221 AA.  
 ID Q9ESK1  
 AC Q9ESK1;  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Putative G-protein coupled receptor GPCR14 (Fragment).  
 GN Name=Gpcr14;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Harian Sprague-Dawley;  
 RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;  
 RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AF090348; AAG24470.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein-coupled receptor protein signaln. . .; IEA.  
 DR InterPro; IPR005382; CC 10 receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR01557; CHEMOKINER10.  
 DR PRINTS; PR00237; GPCR\_RHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 221 221  
 FT SEQUENCE 221 AA; 24342 MW; 5622D6073738A6C CRC64;  
 SQ

Query Match 50.1%; Score 912; DB 2; Length 221;  
 Best Local Similarity 83.3%; Pred. No. 3e-48;  
 Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 96 FFAVNAVHGVLTGKIMCKITTSALTYLNFSGMQFLACISIDRYVAVTKVPSQSGVGKPCW 155  
 DB 19 FFAVNAVHGMIIIGKMKCKVTSALYTNFVSGMQLACISIDRYVAITKAPSGSGVGKPCW 78  
 QY 156 IICFCVMAAILLSIPQLVFTYNDNARCIPIPRVLTGSMKALIQMLEICIGFVVPFLI 215  
 DB 79 IICCCWTAALISTIQQLVFTYNNARCTPVFPHLIGTSKASIQMLEIFIGFVVPFLI 138  
 QY 216 MGVCFITARTLMKMNINIKISRLKVLTVVIVITQLPYNIYVKFCRAIDIIYSLTSG 275  
 DB 139 MGVCFAMTARKLIKMNIKSRRLRLVLAVVVFTRLPYNVVVKCGQALDAIYLLITNC 198  
 QY 276 NMSKRMDAIQVTESTIALFHSCL 298  
 DB 199 DMSKRMVAIODESTIALFHSCL 221

## RESULT 8

Q6YT47 PRELIMINARY; PRT; 369 AA.  
 ID Q6YT47  
 AC Q6YT47;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Chemokine (C-C motif) receptor 9 isoform A (Chemokine C-C motif receptor 9).  
 GN Name=CCR9;

OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 OC NCBI\_TaxId=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Muneta Y., Uenishi H.;  
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T., Uenishi H.;  
 RL Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AP06184; BAD08643.1; -.  
 DR EMBL; AB119263; BAD12126.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein-coupled receptor protein signaln. . .; IEA.  
 DR InterPro; IPR004069; CC 9 receptor.  
 DR InterPro; IPR000355; Cmkline\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01531; CHEMOKINER9.  
 DR PRINTS; PR00237; GPCR\_RHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 369 AA; 41967 MW; DEBF76538600620 CRC64;

Query Match 36.4%; Score 663; DB 2; Length 369;  
 Best Local Similarity 38.4%; Pred. No. 6.5e-33;  
 Matches 129; Conservative 68; Mismatches 117; Indels 22; Gaps 5;

QY 2 ALEQNSTDYEEENMGNTDYDQY---ELICIKEDVREFAKVPFLVLTIVFVIGLAG 58  
 DB 8 SLMPNMPDYGXDARP--SIEDYGNFTFDLCKKNHVGQFHSHPFLPYMLVFIYGANG 65  
 QY 59 NSMVVAIYVYKKQRTKTDVYLNLAVDILLFTLPFAVNAVHGVLTGKIMCKITTSAL 118  
 DB 66 NSLVILVYVYCTRVKTMDFLNLADLLVLPFAVNAADQMKQRTCKVKNVSM 125  
 QY 119 YTLNFPVSGMQLACISIDRYVAVTKVPSQSGVGKPCW-----IICFCVMAAILLS 169  
 DB 126 YKNNFYSVLLTMCISVDRIYIAIQ---AVRAQTRQKRLLYSKVCFYVWMAALC 180  
 QY 170 IFQLVFVTV---NDNARCIPIPRVLTGSMKALIQMLEICIGFVVPFLIMGVCFITART 226  
 DB 181 IPELILSYQKEHDAICMNVYPSDESTNLKSAVLTKVILGFLPFVWMACTYIIHT 240  
 QY 227 LMKMPNIKISRLKVLTVVIVITQLPYNIYVKFCRAIDIIYSLTSCMSGRMDIAIQ 286  
 DB 241 LIOAKKSSGHKALKVITIVLFTVFLVLSQFPYNCGLAQITDAYTMFISCAVSTNDICQ 300  
 QY 287 VTESIALFHSCLNPIITVPMGASPKYVWMAKVKXG 322  
 DB 301 VTQTLAFFFHSCNPIVTVFVGERFRDLVTKLNILG 336

## RESULT 9

CKR7\_HUMAN STANDARD; PRT; 378 AA.  
 ID CKR7\_HUMAN  
 AC P32248;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7) (MIP-3 beta receptor) (BBV-induced G protein-coupled receptor 1) (BB1) (BLR2).  
 DE (BB1) (BLR2).



GN Name=CCR7; Synonyms=CMKCR7, EB01, EV01;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93180173; PubMed=8383338;  
RA Birkenbach M.P., Josefsen K., Yalamanchilli R.R., Lenoir G.M.,  
RT Kieff E.;  
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G  
RT protein-coupled peptide receptors.";  
RL J. Virol. 67:2205-2220(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=95154835; PubMed=7851893;  
RA Schweickart V.L., Raport C.J., Godiska R., Byers M.G., Eddy R.L. Jr.,  
RA Shows T.B., Gray P.W.;  
RT "Cloning of human and mouse EB01, a lymphoid-specific G-protein-  
RT coupled receptor encoded on human chromosome 17q12-q21.2.";  
RL Genomics 23:643-650(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=922388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Vedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,  
RA Villalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.C., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallov D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator  
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in various lymphoid tissues and  
CC activated B and T lymphocytes, strongly up-regulated in B cells  
CC infected with Epstein-Barr virus and T cells infected with  
CC herpesvirus 6 or 7.  
CC -1- INDUCTION: By EBV.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC -----  
DR EMBL; L08176; AAA58615.1; -;  
DR EMBL; L31584; AAA74230.1; -;  
DR EMBL; L31583; AAA74230.1; JOINED.  
DR EMBL; L31583; AAA74230.1; JOINED.  
DR EMBL; L31581; AAA74231.1; -;  
DR EMBL; BC035343; AAH35343.1; -;  
DR PIR; A45680; A45680.  
DR PIR; B55735; B55735.  
DR HSSP; P34996; 1DDD.

Query Match	Best Local Similarity	Score 659;	DB 1;	Length 378;
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7;
DR	Genev; HGNC:1608; CCR7.			
DR	MIM; 600242; -			
DR	GO; GO:0005887; C:Integral to plasma membrane; TAS.			
DR	GO; GO:0004950; F:Chemokine receptor activity; TAS.			
DR	GO; GO:0004930; F:G-protein coupled receptor activity; TAS.			
DR	GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . . ; TAS.			
DR	GO; GO:0006935; P:chemotaxis; TAS.			
DR	GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.			
DR	GO; GO:0006954; P:inflammatory response; TAS.			
DR	InterPro; IPR001718; CC_7_receptor.			
DR	InterPro; IPR000355; Chemkine_receptor.			
DR	InterPro; IPR000276; GPCR_Rhodopn.			
DR	Pfam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHOPOSN			
DR	PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_REC_P2_1; 1.			
KW	G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.			
FT	SIGNAL	1	24	Potential.
FT	CHAIN	25	378	C-C chemokine receptor type 7.
FT	DOMAIN	25	59	Extracellular (Potential).
FT	TRANSMEM	60	86	1 (Potential).
FT	DOMAIN	87	95	Cytoplasmic (Potential).
FT	TRANSMEM	96	116	2 (Potential).
FT	DOMAIN	117	130	Extracellular (Potential).
FT	TRANSMEM	131	152	3 (Potential).
FT	DOMAIN	153	170	Cytoplasmic (Potential).
FT	TRANSMEM	171	191	4 (Potential).
FT	DOMAIN	192	219	Extracellular (Potential).
FT	TRANSMEM	220	247	5 (Potential).
FT	DOMAIN	248	263	Cytoplasmic (Potential).
FT	TRANSMEM	264	289	6 (Potential).
FT	DOMAIN	290	313	Extracellular (Potential).
FT	TRANSMEM	314	331	7 (Potential).
FT	DOMAIN	332	378	Cytoplasmic (Potential).
FT	CARBOHYD	36	36	N-linked (GLCNAC. . . ) (Potential).
FT	DISULFID	129	210	By similarity.
FT	CONFLICT	182	183	IW -> SA (in Ref. 1).
FT	CONFLICT	337	337	L -> I (in Ref. 1).
SEQ	SEQUENCE	378 AA;	42874 MM;	DACBA213841ABD4 CRC64;
Query Match	Best Local Similarity	Score 659;	DB 1;	Length 378;
Matches 144;	Conservative 66;	Mismatches 124;	Indels 38;	Gaps 7;
OY	1	MALBONOSTDYVEENENMGVDSOVELICIKEDVEEFAKFLPVETLTVFVIGLAGNS	60	
DB	21	VCLCODEVTDYIDQNT---TDVTLFESLCSKDVANFKRFLPIMYSIIICPGLGNG	77	
OY	61	MYVAIYVYKQRTKTDVYIILNLAVALDLLFTLPEAVANVHGVLAGIMCKITSALYT	120	
DB	78	LVLVLTLYIFKRLKMTDTYLLNLNLAVALDILFTLTPFAVYSAKSMVGVECFKLIPIAYK	137	
OY	121	LNPFSGMQLACSIDRYVNAVTKPS---QSGGKRCWIIICPVMMAAIILSTPOLVEY	176	
DB	138	MSFSPSGMLLLCISIDRYVNAVQVSAHRHRAVLLISKSCVGIWMLATVATSLPELVS	197	
OY	177	TVNDNA-----RCIPIPRYLGISMKALLQMLEICIGFVVPFLMGVCYPTARTLMKP	231	
DB	198	DLQSSSEBQANRGSLIEH---VEAFITIQAVQWVIFLVPDLAMSCYLVIITLLQAR	254	
OY	232	NIKLSRPLKULLTVVYIFVITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQVETI	291	
DB	255	NFENRKAIKYIAVAVVFIQOLFYNQVLAQIVANFNITSTSELKOLNIADVYSL	314	
OY	292	ALFHSCLNPILYVEMGASFKNYVWKVAKKG-----SW-----RPROSVSEFPDP	337	
DB	315	ACVACCNPFYAIAYIGYKFRNDLFKLKDKDGLCSQEDLRQMSGCRHIRBSMSVE-----	369	
OY	338	SEGTEPTSTFS	349	
DB	370	----AETTTFS	377	

## RESULT 10

06YT46 PRELIMINARY; PRT; 357 AA.  
 AC 06YT46;  
 DT 05-JUL-2004 (Tremblrel. 27, Created)  
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Chemokine (C-C motif) receptor 9 isoform B.  
 GN Name=CCR9;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shikata H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AB006184; BAD08644.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR004069; CC 9 receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1, 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR01531; CHEMOKINER9.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPE\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPE\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 357 AA; 40725 MW; 93F80F90F91337A CRC64;

## Query Match 36.1%; Score 657; DB 2; Length 357;

Best local Similarity 38.7%; Pred. No. 1.5e-32;  
 Matches 127; Conservative 67; Mismatches 112; Indels 22; Gaps 5;

QY 10 DYYEENEMNGTYDYSQY---ELICTKEDREFAKYFLPVFLTFVFIAGLSNMYVAIY 66  
 DB 4 DYGVDATP--SIEDYNGFTFDLFCCKNHYRCFASHFLPLVYLVEIVGAVNSLVILVY 61  
 QY 67 AYYKKORTKTDVYVILNLAVALDLLFTLPFWAVNAHGWVLGKIMCKITSALTNLFPVSG 126  
 DB 62 WYCTKRYKTMDFMLNLALADLFLVTLPPWALAADQMKFQTFCKKVNMSYKMPYSC 121  
 QY 127 MQLACISIDRYVAVTVPSSQSGVGRPCW-----IICFCVMAAAILLSIPQLVFYT 177  
 DB 122 VLLIMKISDRIYALNQ-----AMRAQITWRQKRLYSKLVCFVWMAALCIPELLVSG 176  
 QY 178 V--NDNARCIPIEPYRLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLTKMKNIT 234  
 DB 177 VKEHHAICTWYYPDESGTNLSAVLTKVILGFFELPFVMAACVYIIIIHTLIQAKKS 236  
 QY 235 ISRLPLVLLVTVVFIQTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQTESIATLF 294  
 DB 237 KKHALKVTVLTVFVLSOPFNVCVLLVQITIDAYTMTFISCAVSTINDICFOVLTITAF 296  
 QY 295 HSCINPLLYFMGASFKNYMKVAKKYG 322  
 DB 297 HSCINPLVLYFVGFRFRDLVTKLNLG 324

## RESULT 11

08HZR6 PRELIMINARY; PRT; 378 AA.  
 AC 08HZR6;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

## DE CC chemokine receptor 7.

GN Name=CCR7;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=22471764; PubMed=12406887; DOI=10.1182/Blood-2002-08-2653;  
 RA Choi Y.K., Falter B.A., Murphy-Corb M.A., Reinhardt T.A.;  
 RT "Simian immunodeficiency virus dramatically alters expression of  
 RT homeostatic chemokines and dendritic cell markers during infection in  
 RT vivo."  
 RL Blood 101:1684-1691(2003).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; AF508731; AA047099.2; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR001718; CC\_7\_receptor.  
 DR InterPro; IPR000355; Chmkine\_receptor.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1, 1.  
 DR PRINTS; PR00657; CCHEMOKINER.  
 DR PRINTS; PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPE\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPE\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 378 AA; 42876 MW; D031B84829F08EF CRC64;

## Query Match 36.1%; Score 657; DB 2; Length 378;

Best local Similarity 38.9%; Pred. No. 1.5e-32;  
 Matches 143; Conservative 65; Mismatches 122; Indels 38; Gaps 7;

QY 5 ONOSTDYEEENEMNGTYDSQYELICTKEDREFAKYFLPVFLTFVFIAGLSNMYVA 64  
 DB 25 QDEVDYDYGDN--TVDTYLPESLCSKQDVANFAMFLPTMYSILICVGLGKGLVVL 81  
 QY 65 IYAYKKORTKTDVYVILNLAVALDLLFTLPFWAVNAHGWVLGKIMCKITSALTNLVNFV 124  
 DB 82 TVIYFRLKTMTDVYVILNLAVALDILFTLPFWAASAASWVGAFKLIPTAYTMSPF 141  
 QY 125 SGMLPLACISIDRYVAVTVPSS--QSGVGKPCWITCCVMAAAILLSIPQLVFYTVD 180  
 DB 142 SGMLPLACISIDRYVAIVQAVSAHRHRAVLLISKLSGVILATVLSIPELLVSGLQR 201  
 QY 181 NA-----RCIPPIEPYRLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLTKMKNIT 235  
 DB 202 SSSEQAMRCSLITEN--VEAFITIOVAGMVGFLVPLAMSFYVITRTILQANRFR 258  
 QY 236 SBLPLKTLTVVTVFVITQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQTESIATLF 295  
 DB 259 NKAIKYIIVVTVFVITQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQTESIATLF 318  
 QY 296 SCINPLIYFMGASFKNYMKVAKKYG-----SW-----RRQROVEEFPFSPSE 341  
 DB 319 CCVNPFLVAFIGVGRFNDLFLKFDJGCLSOBQLROMSCHRIRRSMSVE----- 369  
 QY 342 TEPTSTPS 349  
 DB 370 AETTTTFS 377

## RESULT 12

CKR7 MOUSE STANDARD; PRT; 378 AA.  
 ID CKR7\_MOUSE  
 AC P47774;  
 DT 01-FEB-1996 (Rel. 33, Created)

DT	01-FEB-1996	[Rel. 33, Last sequence update]
DT	25-OCT-2004	[Rel. 45, Last annotation update]
DE	C-C chemokine receptor type 7 precursor (C-C CCR-7) (CC-CR-7) (CCR-7)	
DE	(MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)	
DE	(EBI1).	
GN	Name=Ccr7; Synonym=Cmkbtr7, Ebi1, Ebi1h;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sclerothamnii; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6 X CBA; TISSUE=Thymus;	
RC	MEDLINE=95154835; PubMed=7851893;	
RA	Schweikart V.L., Raport C.J., Godliska R., Byers M.G., Eddy R.L. Jr.,	
RA	Shows T.B., Gray P.W.,	
RT	"Cloning of human and mouse EBI1, a lymphoid-specific G-protein-	
RT	coupled receptor encoded on human chromosome 17q12-q21.2.";	
RL	Genomics 23:643-650(1994).	
CC	-1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator	
CC	of EBV effects on B lymphocytes or of normal lymphocyte functions.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.tsb-sib.ch/announce/">http://www.tsb-sib.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@tsb-sib.ch">license@tsb-sib.ch</a> ).	
CC	-----	
DR	EMBL; L31580; AAA74232.1; .	
DR	PIR; A55735; A55735.	
DR	MGI; MGI:103011; Ccr7.	
DR	GO; GO:0016493; F:C-C chemokine receptor activity; IMP.	
DR	GO; GO:0006935; P:Immune response; IMP.	
DR	InterPro; IPR001718; CC_7_receptor.	
DR	InterPro; IPR000355; Chemkine_receptor.	
DR	InterPro; IPR000276; GPCR_Rhodopsn.	
DR	Pfam; PF00001; 7tm1.1; 1.	
DR	PRINTS; PR00237; GPCR_RHODOPSN.	
DR	PROSITE; PS00237; G_PROTEIN_REC_P1.1; 1.	
DR	PROSITE; PS50262; G_PROTEIN_REC_P1.2; 1.	
KW	G-protein coupled receptor; Glycoprotein; signal; Transmembrane.	
FT	SIGNAL	1
FT	CHAIN	25 378
FT	DOMAIN	25 59
FT	TRANSMEM	60 86
FT	DOMAIN	87 95
FT	TRANSMEM	96 116
FT	DOMAIN	117 130
FT	TRANSMEM	131 152
FT	DOMAIN	153 170
FT	TRANSMEM	171 191
FT	DOMAIN	192 219
FT	TRANSMEM	220 247
FT	DOMAIN	248 263
FT	TRANSMEM	264 289
FT	DOMAIN	290 313
FT	TRANSMEM	314 331
FT	DOMAIN	332 378
FT	CARBOHD	36 36
FT	DISULFD	129 210
SQ	SEQUENCE	378 AA; 42941 MW; ACBIA422CF54AA54 CRC64; By similarity.

```

Query Match 35.7%; Score 650; DB 1; Length 378;
Best Local Similarity 38.3%; Pident.No. 4,1e-32;
Matches 140; Conservative 67; Mismatches 125; Indels 34; Gaps 8.

QY 5 QNOSTDYEEENMGCTDYSGYELICTKEDVRERAPKFLPLVLIVFVIGLAGSMVYA 64
   ||: || || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

```

Db	25	QDEWTDYDIGENNT---TVDYTLYESVCRKDVBRNFKAMFLPLMYSVICFVGLLNGNLVL	81
Qy	65	IYAYKKORTKTDVYIILNLAVADLLLTLPMPVANAHVGVLGKIMCKITSLATYTLANV	124
Db	82	TYIYFKRKTKMTDYLNLMAVADILFLFLILPFMAVSEAKSMIFGVYLCCKGIRGYLSPF	141
Qy	125	SGMGLFACISIDRYAVATKVPSSQS-----VGKPCWICGCVMAAALLSPOLVFT	177
Db	142	SGMLLLCISIDRYAVAIQVAVSRHRHRARVLLISK--LSCYIWMALLFLSIPELLVSG	198
Qy	178	VNDNA-----RCIPFIPRYLGTSMKAL--IQMLEICIGFVVPFLIMGVCFYTTARTLMK	230
Db	199	LQKXSGEDTLKFC-----SLVGAQVREALTIIQVAGVFGELVPMMLMSFCYLIIRLLQA	253
Qy	231	ENIKISREPLKXLLTVYIVFYITOLPYNIVKFCRAIDIIYSLTSCNMSKMDIAIQVTS	290
Db	254	RNFERNKRIKYLIAVVVVVIFVQJPFYNGVVLAQVAFNFINITSSCETSQKLNIAVDVFS	313
Qy	291	IALFHSCLNPLIYVPMGASPFKNYVMKAKKXGSMKOR-----QSVDEFPFDSBGPIE	343
Db	314	LASVRCVCPNPELYAFITGVKFRSSDLFKPKDLGICSGQERLRHWSSCRHRNNAVSME--AE	371
Qy	344	PTSTFS 349	
Db	372	TTTTFS 377	
RESULT 13			
OG6P68:			
ID	OG6P68	PRELIMINARY:	PRT: 358 AA.
AC	OG6P68		
DT	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	MGC80638 protein.		
GN	Name=MGC80638:		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_Taxid=8355;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Splice;		
RC	MEBLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.24260389;		
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RX	Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,		
RX	Altschul S.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,		
RX	Hopkins R.F., Zedberg B., Buetow K.H., Scheefer C.F., Shat N.K.,		
RX	Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,		
RX	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RX	Brownstein M.J., Ugin T.B., Toshitsuki S., Carlinici P., Prange C.,		
RX	Raha S.S., Loeuallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RX	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RX	Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultx S.W.,		
RX	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RX	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RX	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RX	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RX	Rodriguez R.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,		
RX	Kirylushki M.I., Skalska U., Smalite D.E., Schnerch A., Schein J.E.,		
RX	Jones S.J., Marz M.A.;		
RX	"Generation and initial analysis of more than 15,000 full-length human		
RL	and mouse cDNA sequences.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16859-16903 (2002).		
RT	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Splice;		
RC	MEBLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;		
RX	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,		
RX	Richardson P.,		
RT	"genetic and genomic tools for Xenopus research: The NIH Xenopus		
RT	initiative."		



DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00657; CCHEMOKINER.  
 DR PRINTS: PR00641; CHEMOKINER7.  
 DR PRINTS: PR00237; GPCRKHODOPN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW SEQUENCE 378 AA; 42855 MW; F027451989B59683 CRC64;

Query Match 35.6%; Score 648; DB 2; Length 378;  
 Best Local Similarity 38.6%; Pred. No. 5.5e-32;  
 Matches 140; Conservative 67; Mismatches 128; Indels 28; Gaps 7;

QY 5 QNOSTDYEEENMGTYDYSQYELICIKEDYREPAKVFPLPVLTIVFVIGLAGNSMVYA 64  
 DB 25 QDEVTDDYIGENT---TVDYTLYESVCFKDVNRKAMFLPLMYSVICFVGLGNGLVYL 81  
 QY 65 IYAYKKORTKTDVYILNLAVDLLFTLPFWANAVAHGVLGKIMKITSALYTLNFV 124  
 DB 82 TYIYKRLKMTDVTYILNLAVDILFLMLPFWAYSEAKSWIFGAYLCKSIGIYKLSFF 141  
 QY 125 SGMQFLACISIDRYAVAVTKVPS---QSGVGKPCWICPCVMAAILLSIPOLVFYTVND 180  
 DB 142 SGMILLICISIDRYAVAVTKVPS---QSGVGKPCWICPCVMAAILLSIPOLVFYTVND 201  
 QY 181 NA-----RCIPFPYRLGTSMAKAL--IQMLEICIGFVVPFLIMGVCFITARTLMKMPYI 233  
 DB 202 NSGEDTLRC-----SLVSAQVEALITTVQAQVGFVPLMLMSPCYLVIIRTLQARNF 256  
 QY 234 KISRPLKVLTVYIVFYITQLPYNIYVFCRAIDIIYSLTSCNMSKMDIAIQVETSL 293  
 DB 257 ERNKAIKYIAVAVVFFVQLPYNGVLAQTVANFNITNSCETSQOLNIAVDYISLAS 316  
 QY 294 FHSCLNPLIYVFMGASFKNYVMKAKYGSWROR-----QSVKEPFDESGPTPTS 346  
 DB 317 VRCVNPFLYAFITGVKFRSDLPFLFDLQCLSGERLRHWSSCRHYANASVSM--AETTT 374  
 QY 347 TFS 349  
 DB 375 TFS 377

## RESULT 15

Q6U2D6 PRELIMINARY; PRT; 378 AA.  
 AC Q6U2D6;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Chemokine receptor 7-like protein.  
 GN Name=Ccr7;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RC STRAIN=BN; TISSUE=Lymph node;  
 RA Quintini G., Voland B., Hoffmeyer A.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL: AY379972; AKR24573.1; -  
 DR GO: GO:0016021; C:Integral to membrane; IEA.  
 DR GO: GO:0016493; P:C-C chemokine receptor activity; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signaling; IEA.  
 DR InterPro: IPR001718; CC\_7\_receptor.  
 DR InterPro: IPR000355; ChmKine\_receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopn.  
 DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00657; CCHEMOKINER.

DR PRINTS: PR00641; CHEMOKINER7.  
 DR PRINTS: PR00237; GPCRKHODOPN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Receptor; Transmembrane.  
 KW SEQUENCE 378 AA; 42821 MW; A015E711DC4B521F CRC64;

Query Match 35.5%; Score 646; DB 2; Length 378;  
 Best Local Similarity 38.0%; Pred. No. 7.2e-32;  
 Matches 138; Conservative 68; Mismatches 129; Indels 28; Gaps 7;

QY 5 QNOSTDYEEENMGTYDYSQYELICIKEDYREPAKVFPLPVLTIVFVIGLAGNSMVYA 64  
 DB 25 QDEVTDDYIGENT---TVDYTLYESVCFKDVNRKAMFLPLMYSVICFVGLGNGLVYL 81  
 QY 65 IYAYKKORTKTDVYILNLAVDLLFTLPFWANAVAHGVLGKIMKITSALYTLNFV 124  
 DB 82 TYIYKRLKMTDVTYILNLAVDILFLMLPFWAYSEAKSWIFGAYLCKSIGIYKLSFF 141  
 QY 125 SGMQFLACISIDRYAVAVTKVPS---QSGVGKPCWICPCVMAAILLSIPOLVFYTVND 180  
 DB 142 SGMILLICISIDRYAVAVTKVPS---QSGVGKPCWICPCVMAAILLSIPOLVFYTVND 201  
 QY 181 NA-----RCIPFPYRLGTSMAKAL--IQMLEICIGFVVPFLIMGVCFITARTLMKMPYI 233  
 DB 202 NSGEDTLRC-----SLVSAQVEALITTVQAQVGFVPLMLMSPCYLVIIRTLQARNF 256  
 QY 234 KISRPLKVLTVYIVFYITQLPYNIYVFCRAIDIIYSLTSCNMSKMDIAIQVETSL 293  
 DB 257 ERNKAIKYIAVAVVFFVQLPYNGVLAQTVANFNITNSCETSQOLNIAVDYISLAS 316  
 QY 294 FHSCLNPLIYVFMGASFKNYVMKAKYGSWROR-----QSVKEPFDESGPTPTS 346  
 DB 317 VRCVNPFLYAFITGVKFRSDLPFLFDLQCLSGERLRHWSSCRHYANASVSM--AETTT 374  
 QY 347 TFS 349  
 DB 375 TFS 377

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